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191509

From: Hamud, Fozia
Sent: Wednesday, May 31, 2006 1:28 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 10/732,796

URFB

Kindly search SEQ ID NOs: 11 and 12 of 10/732,796 against commercial and interference data bases. thank you.

FOZIA HAMUD
PATENT EXAMINER
ART UNIT 1647
ROOM: REM 4D64
MAIL BOX: REM 4C70

Noted

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 2, 2006, 22:53:51 ; Search time 52 Seconds
(without alignments)
1339.892 Million cell updates/sec

Title: US-10-732-796a-12

Perfect score: 4154

Sequence: 1 MTKDKEPIVKSHPVCLMII.....IRAFNMKLTIVENNVDYS 796

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

1: /EMC Celera SIDS3/ptodata/2/1aa/5 COMB pep: *
2: /EMC Celera SIDS3/ptodata/2/1aa/6 COMB pep: *
3: /EMC Celera SIDS3/ptodata/2/1aa/7 COMB pep: *
4: /EMC Celera SIDS3/ptodata/2/1aa/H COMB pep: *
5: /EMC Celera SIDS3/ptodata/2/1aa/PTUS COMB pep: *
6: /EMC Celera SIDS3/ptodata/2/1aa/RE COMB pep: *
7: /EMC Celera SIDS3/ptodata/2/1aa/backfilest pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4154	100.0	802	US-09-949-002-512	Sequence 512, App
2	4149	99.9	796	US-09-949-002-386	Sequence 386, App
3	2830	68.1	786	US-09-949-002-351	Sequence 351, App
4	2459	59.2	672	US-09-949-002-522	Sequence 522, App
5	1905.5	45.9	811	US-09-991-181-57	Sequence 57, App
6	1905.5	45.9	811	US-09-990-444-57	Sequence 57, App
7	1905.5	45.9	811	US-09-997-333-57	Sequence 57, App
8	1905.5	45.9	811	US-09-992-598-57	Sequence 57, App
9	1905.5	45.9	811	US-09-989-735-57	Sequence 57, App
10	1905.5	45.9	811	US-09-989-728-57	Sequence 57, App
11	1905.5	45.9	811	US-09-997-514-57	Sequence 57, App
12	1905.5	45.9	811	US-09-989-728-57	Sequence 57, App
13	1905.5	45.9	811	US-09-997-349-57	Sequence 57, App
14	1905.5	45.9	811	US-09-997-653-57	Sequence 57, App
15	1905.5	45.9	811	US-09-989-293A-57	Sequence 57, App
16	940	22.6	784	US-09-982-308B-23	Sequence 23, App
17	837	20.1	775	US-09-949-016-8799	Sequence 8799, App
18	504	12.1	739	US-09-396-985B-4	Sequence 4, App
19	504	12.1	739	US-09-396-985B-2	Sequence 2, App
20	504	12.1	839	US-09-396-985B-98	Sequence 98, App
21	504	12.1	844	US-09-949-016-9438	Sequence 9438, App
22	496	11.9	1059	US-09-954-987B-187	Sequence 187, App
23	488.5	11.8	1041	US-09-999-933A-498	Sequence 498, App
24	488.5	11.8	1041	US-09-954-987B-184	Sequence 184, App
25	488.5	11.8	1041	US-09-954-987B-186	Sequence 186, App
26	488.5	11.8	1041	US-10-020-445A-498	Sequence 498, App

27	488.5	11.8	1041	US-09-978-189-498	Sequence 498, App
28	488.5	11.8	1041	US-10-017-085A-498	Sequence 498, App
29	488.5	11.8	1041	US-10-145-129A-498	Sequence 498, App
30	488.5	11.8	1041	US-10-013-929A-498	Sequence 498, App
31	488.5	11.8	1041	US-10-013-917A-498	Sequence 498, App
32	481.5	11.6	904	US-09-949-002-352	Sequence 352, App
33	481.5	11.6	910	US-09-949-002-352	Sequence 352, App
34	449.5	10.8	1049	US-09-954-987B-172	Sequence 172, App
35	446.5	10.7	1049	US-09-999-833A-496	Sequence 496, App
36	446.5	10.7	1049	US-09-954-987B-170	Sequence 170, App
37	446.5	10.7	1049	US-10-020-445A-496	Sequence 496, App
38	446.5	10.7	1049	US-09-978-189-496	Sequence 496, App
39	446.5	10.7	1049	US-10-017-085A-496	Sequence 496, App
40	446.5	10.7	1049	US-10-145-129A-496	Sequence 496, App
41	446.5	10.7	1049	US-10-013-929A-496	Sequence 496, App
42	446.5	10.7	1049	US-10-013-917A-496	Sequence 496, App
43	444.5	10.7	1050	US-09-954-987B-175	Sequence 175, App
44	444.5	10.7	989	US-09-954-987B-171	Sequence 171, App
45	441.5	10.6	835	US-09-396-985B-6	Sequence 6, App

ALIGNMENTS

RESULT 1	US-09-949-002-512	US-09-949-002-512
Sequence 512, Application	US/09949002	
Patent No. 6900016		
GENERAL INFORMATION:		
APPLICANT: VENTER, J. Craig et al.		
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION		
TITLE OF INVENTION: AND USES THEREOF		
FILE REFERENCE: CLO00790		
CURRENT APPLICATION NUMBER: US/09/949,002		
PRIOR FILING DATE: 2000-01-28		
PRIOR APPLICATION NUMBER: 60/231,401		
PRIOR FILING DATE: 2000-09-08		
NUMBER OF SEQ ID NOS: 10823		
SOFTWARE: FASTSEQ for Windows Version 4.0		
SEQ ID NO 512		
LENGTH: 802		
TYPE: PRT		
ORGANISM: Human		
US-09-949-002-512		
Query Match	100.0%; Score 4154; DB 2; Length 802;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 796; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MTKDKEPIVKSHPVCLMIIIVGTRIQPSDGNFAVDKSKRGLIHVPKDLPLKTKVLDMS 60	
DB	7 MTKDKEPIVKSHPVCLMIIIVGTRIQPSDGNFAVDKSKRGLIHVPKDLPLKTKVLDMS 66	
QY	61 QNYIAELQSDMSFSELTVLRLSNRIQDLDSVFKPNODELYDLSNOLKISCHPI 120	
DB	67 QNYIAELQSDMSFSELTVLRLSNRIQDLDSVFKPNODELYDLSNOLKISCHPI 126	
QY	121 VSFRLDLSFNDFKALPICKERGNLSQNLFLGLSAMKQKDLPLIAHLASYYILLDLRN 180	
DB	127 VSFRLDLSFNDFKALPICKERGNLSQNLFLGLSAMKQKDLPLIAHLASYYILLDLRN 186	
QY	181 YIKENETESLQILNAKTLHLVHPRTSLPAIVNISVNTLGLQTLTKLNDNCQVFLK 240	
DB	187 YIKENETESLQILNAKTLHLVHPRTSLPAIVNISVNTLGLQTLTKLNDNCQVFLK 246	
QY	241 FLSLSTRSTLNLFTLNHIEETWKCLVRFQFLMPKPEYVNIYVLTIIIESIREDFYTS 300	
DB	247 FLSLSTRSTLNLFTLNHIEETWKCLVRFQFLMPKPEYVNIYVLTIIIESIREDFYTS 306	
QY	301 KTKLKALTIETHTNOVFLFSQALATVPSSENMIMLTISDPFIHMLCPHAPSTFKFLNF 360	
DB	307 KTKLKALTIETHTNOVFLFSQALATVPSSENMIMLTISDPFIHMLCPHAPSTFKFLNF 366	

QY 361 TONVFTDSIFPKCSITLVKLETLIIQKNGIKDLFKVGLMTKOMPSEIIDVSNWSLESGRH 420
DB 367 TONVFTDSIFPKCSITLVKLETLIIQKNGIKDLFKVGLMTKOMPSEIIDVSNWSLESGRH 426
QY 421 KENCWVSIIVLNLSSNMULTDSVFRCLPPIIKVLDHSNKIKSVPKQVVKLEALQELNV 480
DB 427 KENCWVSIIVLNLSSNMULTDSVFRCLPPIIKVLDHSNKIKSVPKQVVKLEALQELNV 486
QY 481 AFNSLTDLPGCGSFSSLSVLIIIDHNSVSHPSADFFQSCQKRSIYAGDNPFQCTCELERF 540
DB 487 AFNSLTDLPGCGSFSSLSVLIIIDHNSVSHPSADFFQSCQKRSIYAGDNPFQCTCELERF 546
QY 541 VKNIDVSSSEVLGMPDYSKCDYPESYRGSPDKDFHMSLSCNTLLIYTGATMLVLAV 600
DB 547 VKNIDVSSSEVLGMPDYSKCDYPESYRGSPDKDFHMSLSCNTLLIYTGATMLVLAV 606
QY 601 TVTSLCTIYLDLPWYLRMCQWOTQRRRANIPLEELQNLQPHAFISYSEHDSAMVKSSEL 660
DB 607 TVTSLCTIYLDLPWYLRMCQWOTQRRRANIPLEELQNLQPHAFISYSEHDSAMVKSSEL 666
QY 661 VPYLEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSIYVLSPPNVQSEWCHYELYPAH 720
DB 667 VPYLEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSIYVLSPPNVQSEWCHYELYPAH 726
QY 721 HNLPHGSGNNLILILLEPIPNKHYKHLKALMTORTYLOMPKSKRGFLFMANIRAA 780
DB 727 HNLPHGSGNNLILILLEPIPNKHYKHLKALMTORTYLOMPKSKRGFLFMANIRAA 786
QY 781 FNMKLTIVTENNDVKS 796
DB 787 FNMKLTIVTENNDVKS 802

RESULT 2

US-09-949-002-386
; Sequence 386, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 386
; LENGTH: 796
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-386

Query Match 99.9%; Score 4149; DB 2; Length 796;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTQKKEPIVKSFFHVCMLIIIVGTRIQFSDGNEFAVDSKRGILHVPKDLPLKTYVLDMS 60
DB 1 MTQKKEPIVKSFFHVCMLIIIVGTRIQFSDGNEFAVDSKRGILHVPKDLPLKTYVLDMS 60
QY 61 QNYIAELOVSDMSFSELTVLRLSHNRIOQLDLISVFKFNODLEYDLDSINOQKISCHPI 120
DB 61 QNYIAELOVSDMSFSELTVLRLSHNRIOQLDLISVFKFNODLEYDLDSINOQKISCHPI 120
QY 121 VSPRHLDSFNDPKALPTICKERGNLSQNLFLGISAMKLOKDLPLPAHHLIYIILDLRN 180
DB 121 VSPRHLDSFNDPKALPTICKERGNLSQNLFLGISAMKLOKDLPLPAHHLIYIILDLRN 180
QY 181 YYIKENETESIQILNAKTLHLVFPHTSLFAIQVNISVNTLGLQLTNIKLNDNCQVPIK 240

DB 181 YYIKENETESIQILNAKTLHLVFPHTSLFAIQVNISVNTLGLQLTNIKLNDNCQVPIK 240
QY 241 FLSLETRSTLNFNLNFIETWKLAVFOFLMPKPEYININYLATIIIESIREDFYYS 300
DB 241 FLSLETRPTLNLNFIETWKLAVFOFLMPKPEYININYLATIIIESIREDFYYS 300
QY 301 KTTLKALTIIEHTNQVFLFSQALYTVFSEKNIIMMLTISDPFIHMLCPHAPSTKFLNF 360
DB 301 KTTLKALTIIEHTNQVFLFSQALYTVFSEKNIIMMLTISDPFIHMLCPHAPSTKFLNF 360
QY 361 TONVFTDSIFPKCSITLVKLETLIIQKNGIKDLFKVGLMTKOMPSEIIDVSNWSLESGRH 420
DB 367 TONVFTDSIFPKCSITLVKLETLIIQKNGIKDLFKVGLMTKOMPSEIIDVSNWSLESGRH 426
QY 421 KENCWVSIIVLNLSSNMULTDSVFRCLPPIIKVLDHSNKIKSVPKQVVKLEALQELNV 480
DB 427 KENCWVSIIVLNLSSNMULTDSVFRCLPPIIKVLDHSNKIKSVPKQVVKLEALQELNV 486
QY 481 AFNSLTDLPGCGSFSSLSVLIIIDHNSVSHPSADFFQSCQKRSIYAGDNPFQCTCELERF 540
DB 487 AFNSLTDLPGCGSFSSLSVLIIIDHNSVSHPSADFFQSCQKRSIYAGDNPFQCTCELERF 546
QY 541 VKNIDVSSSEVLGMPDYSKCDYPESYRGSPDKDFHMSLSCNTLLIYTGATMLVLAV 600
DB 547 VKNIDVSSSEVLGMPDYSKCDYPESYRGSPDKDFHMSLSCNTLLIYTGATMLVLAV 606
QY 601 TVTSLCTIYLDLPWYLRMCQWOTQRRRANIPLEELQNLQPHAFISYSEHDSAMVKSSEL 660
DB 607 TVTSLCTIYLDLPWYLRMCQWOTQRRRANIPLEELQNLQPHAFISYSEHDSAMVKSSEL 666
QY 661 VPYLEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSIYVLSPPNVQSEWCHYELYPAH 720
DB 667 VPYLEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSIYVLSPPNVQSEWCHYELYPAH 726
QY 721 HNLPHGSGNNLILILLEPIPNKHYKHLKALMTORTYLOMPKSKRGFLFMANIRAA 780
DB 727 HNLPHGSGNNLILILLEPIPNKHYKHLKALMTORTYLOMPKSKRGFLFMANIRAA 786
QY 781 FNMKLTIVTENNDVKS 796
DB 787 FNMKLTIVTENNDVKS 802

RESULT 3

US-09-949-002-351
; Sequence 351, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 351
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-351

Query Match 68.1%; Score 2830; DB 2; Length 786;
Best Local Similarity 69.5%; Pred. No. 1e-262;

Matches 540; Conservative 92; Mismatches 143; Indels 2; Gaps 1;

QY 12 FHFVCLMIIIVGTRIQFSDGNEFAVDSKRGILHVPKDLPLKTYVLDMSQNYIAELOVSD 71
DB 5 FHFVCLMIIIVGTRIQFSDGNEFAVDSKRGILHVPKDLPLKTYVLDMSQNYIAELOVSD 71

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC53
CURRENT FILING DATE: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 45.9%; Score 1905.5; DB 2; Length 811;

Best Local Similarity 47.8%; Pred. No. 8,2e-174; Matches 382; Conservative 145; Mismatches 251; Indels 21; Gaps 10;

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QY 8 IYKSFHFVCLMIIY-GTRIQFSDGNEFVADSKRGLIHVPKDLPLKTVLDMSONYIAE 66
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DB 3 LIRNIYFICSIWMTAGDAPELPEBEELMTNCSNMSLRKVPADLPATTTLDLSVYLHQ 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 LOVDSMFSISETLVRLSHNRIOQLDLSVFKENODLEYLDLSHNOLOKISCHPIYSFRHL 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 63 IQSSDFHSYVKRLVLLCHNRIOQLDLKTFEENKEIRYIDLNNRILKSTVWYLLAGRLYL 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 127 DISFDFKALPICKEKGNSQLNPLGLSAMKLOKDLPLAHHLISYLLDLRNYIKEN 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 123 DISFDFDMPTICEEAGNMSHLEIIGLSAKIQKSDFOKIAHLMLTVFLGFRTP-LPHY 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 187 ETESQILNAKTLHVFHPTSLFAIOVNISVNTLGLQTLNKLNDNCQVFIKFLSELT 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 181 EEGSLPIINTKTLHVLPMWTFWVILRIGIKITSKLEMTNT----DGKSQVSY--LPHY 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 247 RGSSTLN----FTLNHETWKLCLVRFQFLMPKPEVEYLYNTLT--IESIREEDFTY 299
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 245 RMLSENAKTSVLLINKVDLMDWDLFLILQFWHTSVEHFQIRNVTFGSKAYLDHNSFDY 294
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 300 SKTTLKALIEHTNOVFLFSQALTYVSENNIMMLTSDPRFTIMLCRPHAPSTFKFN 359
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DB 295 SNTVKTSLIEHVHFVFTYIQDKTYLLTKMDIENLTISNOMPMLFPNPTKFOYLN 354
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QY 360 FTQNVFTSIFKRCSTLVLETLILQKNGIKDLFKVGLMTKMPSEILIDVSNLSESGR 419
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 355 FANNILITDELFRKTIQLPHLKTLLNGNKLFTLSIVSCANNTP--LEHIDLQNLQH-X 412
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QY 420 KHEKCTWASIVVNLSSNMLTDSVFRCLPPRAKVLDDLHNSKIKSVKQVYVLEALQELN 479
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DB 413 NDENCSMPETVVNMMISYKRLSDSVFRCLPKSIQIIDLNNNOIQVPEKTIHMLALREIN 472
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QY 480 VAFNSLTLDLPGCGSFSSLSVLLIHDHNSVSHPSADFPQSCQKRSIKAGDNPRQCTCELNE 539
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DB 473 IAFNFLTDLPGCSHRSRLSVLNIENKFIILSPSLDFVQSCQVYVTLNAGNPPRCCTELKN 532
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QY 540 FYKNIDQVSSEVLEKMPDSYKCDYBESYRGSPLKQPFHMSLSNITLLIVTIGATMLVA 599
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 533 FIC-LETYSEVMMVMSYSCTCEYPIINLRGTBLKDVHHELSCTALLIVTIVMLVVG 591
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 600 VVVTSLCITYLDLPWYLRMVCQWTOFRRARBNIPLEBLQNLQFHAFTSYSEHSDAVKSE 659
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 592 LVAFCCLEFDPWYLRMLGQCTQWHRVKTTOEOLKKNVRPHAFISTYSEHSDLVKNB 651
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 660 LVPLYLEKED--IQICHERNFVPGKSIYENIINCIEKSYKSIFFVLSPNFVQSEWCHYEY 717
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 652 LIPNLEKEDGSLICLYESYFDPGKSIENIVSFIKSKSIFVLSPNFVQSEWCHYEY 711
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 718 FAHNHLFHEGNNLILILEPIPNISIPNKYHKLKALMTQRTYLOMPKEKSRGLFWANI 777
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 712 FAHNHLFHENSDBHILILEPIPFYCIPTRYHKLKALLEKKAYLEWPKDRKCGLFWANL 771
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 778 RAAFNNKLLVTYENNDVKS 796
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 772 RAINVNVLATREMYELOQT 790
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RESULT 6
US-09-990-444-57

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; Sequence 57, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC19
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match	45.9%;	Score 1905.5;	DB 2;	Length 811;
Best Local Similarity	47.8%;	Pred. No. 8.2e-174;		
Matches 382;	Conservative 145;	Mismatches 251;	Indels 21;	Gaps 10;

Qy	8	IYVSFHVFCMIITIV-CTRIOFSDGNEPAWDSKGLHVPODLPLKTVLMSQNTYAE	66
Db	3	LIRINIVFCISIVMTABEDAPELPEEBELMTNCSNSLRKVPADLIPATITDLSINLLFQ	62
Qy	67	LQVSDMSFSELTVLRISHNRIOQLDLSVFKENODELYLDSHNOLOKISCHIVSFEHL	126
Db	63	LQSDDFHSVSKVLVLLCHNRIOQLDLKTFEFPKELRYLDSNNMLKSVTMYLAGRLYL	122
Qy	127	LSFENPCKALPICKEGNSQLNFIGLSAMKQKUDLPIALHLSYLLDLRNYIKEN	168
Db	123	LSFENPDMTPICEEAGNSMHEILGLSAGAKIQKSDFOKIALHMLNTVGLGFRY--LPHY	180
Qy	187	ETESLIQILNKAFTLHLVHFPTSLPAIGOVNISVNTLGGLOKTNIKLNDNCOQVFIKLSFLT	240
Db	181	EEBSPLNTKTKHLYLPMDTNFWVLRLDGIKTSKLEMTNI----DGKSQFVSY--EMQ	233
Qy	247	RGSSTLLN----FTLNHIETTKCLVVRVQFPLMPKREVEYLNIYLTJ--IESIREDEPTY	299
Db	235	RNLSLENAKTSVYLLNKKVLDLMDDLFLIQFWHTSVSEHFQIRNVTFGKAKAYLDHNSFDY	294
Qy	300	SKTLTKALTYEHTNQVYLFESQALYTVSENNIMLTSDTPIFHMICPAHSTFKELN	355
Db	295	SNTVMRTIKLEHNFVRFYIQQDKYLLTLTKDDIENLTISNAQMDHMLFPVPTKFOYLN	353
Qy	360	FTQNVFPTDSIFEKCSFLVKELETILIOKNGKODLPKVGLMTKMPSELTDIVSNMSLESGR	418
Db	355	FANNITLDELFRKTIQPLHKLTLINGKLETLSTLVSCEANNTPL--LEHLDLSQÜLDQH-K	412
Qy	420	HKENCTWVESIVLNLSSNNLTDSVFRCLPRLIKYLDLSHNKIKSVKPOVYKLBALQELN	479
Db	413	NDENCSMPETVYVMNNLSYNNKLSDSVFRCLPSKIQIOLDINNNOIQVPRKETHLMALRELN	472
Qy	480	VAENSLTDLPGGSEFSLVLLIDHNSVSHPSADFPQSCQKMRKSKADNFPQCTCEIRE	533
Db	473	IAPNFTLDPRGCHFSRLSVLNIENMFILSPDLDPVQSQEYKTLMAERNFRCCTCEIKN	533
Qy	540	FVNINIDOVSEVLEGMPDSYKCDYRESYVGSPLKDFHMSSELSCNTITLLITVITGATMVLIA	599
Db	533	FIQ-LBEYSSVMMVWGVMSDSTCEYPLANKRGRKLYKHVHLSESCNALLITVIVIMVLVG	591
Qy	600	VTVTSILCYLDLPWYLRAWQWOTRRRARNIPLBELQNTQFNAFISYSEHSDAWKSE	656
Db	592	LAVAFCCILHEDLPWYLRMLGQCQTQTHVRKTKTOQLKRNVPFAFATISYSHSDLSMWKNE	651
Qy	660	LWVYLEKED--IOICHEBNFVPGKISIVNIIINCEKSKYSTFVLSRPNFQSEKCHELY	717
Db	652	LINLEKEDEDSILICYBESYFDPGKISINISVFIKSKYSTFVLSRPNFVQNEWCHAEFY	711
Qy	718	FAHNNLFHEGNSNNLILILEPIPNISIPKRYKALATMOTRYLQWPEKSKRGLFWANI	777
Db	712	FAHNNLFHENSDHIIILILEPIPYCQIPRYRYKLYALLEKAYULEMPDRRCKGLFWANL	771
Qy	778	RAAPNKKLIVTENNDVKS	796
Db	772	RAAINVNVLATREMYELQT	790

RESULT 7
US-09-997-333-57
; Sequence 57, Application US/09997333
; Patent No. 6953836

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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC27
CURRENT APPLICATION NUMBER: US/09/997,333
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 45.9%; Score 1905.5; DB 2; Length 811;
Best Local Similarity 47.8%; Pred. No. 8.2e-174; Indels 21; Gaps 10;
Matches 382; Conservative 145; Mismatches 251;

QY 8 IVKSFHVCIMIIIV-GTRIOFSDONEPAVMSKRGKGLHVDPKDLPLKTKVLDMSQNYAE 66
DB 3 LIRNIYIFCSIVMAKGAPELPEREREIMTCSNMSLRKVRADLPATTTDLSINLLFQ 62
QY 67 LQVSDMSFLSELTVLRLSHNRIOULLDSVFXFNODLEYLDLSHNOLOKISCHPIVSFRL 126
DB 63 LQSDSFHVSVKLRVYLILCHNRIOQLDLDKTFEFNKELRYLDSNNRKLKSVYILAGRLYL 122
QY 127 DISFNDPKALPICKEFGULSQNLFLGSLAMKLOKLDLPIAHHLSTYLLDLRNYYIKEN 186
DB 123 DLSFNDPFTMPICEAGNMSHLEILGSGAKIOKSDFOKIAHLINTVFLGERT--LPHY 180
QY 187 ETESQIINAKTLHLVFPHTSLFAIQVNISVNTLGLQLOTYNIKLNDNCQVFIKFLSELT 246
DB 181 BEGSLPIINTTKLHLVLPMDTNFWVLNRPDGIKTSKILEMTNI---DKSQSFVSY--EMQ 234

QY 247 RGSSTLYN-----FTLNHLEFTWKCIVRVCQFLMPKRPVEAYINVLNT--IESIREEDEFTY 299
 Db 225 RHLSTLENAKTSVLLNKVDLMDLDFLLIQFVHNTSEVHQINNVTPGGCAIYLDHNSFDY 294
 QY 300 SKTYLKALTLTEHTNQVFLPFSQATLVYFSENNIMLTTISDRPFIHMLCEHASTPEKFLN 359
 Db 295 SNTVWRRTIKLEHVHFRVVFYIQODKIKYLLTLTKMDIENLTISNAQMPHLPFNVPFTKQYLN 354
 QY 360 FQONVFTDSIFPEKCSVLVLETLTILQKNGIKLDFKVGMLTKMPSLEILDVSNNSLESGR 419
 Db 355 FANNITLITDELFRKRTIQPLPHAKTLILNGNKLETSLVSCFANNTP-LEHIDLSONLLOH-K 412
 QY 420 HKNENCTWSEIVVLNLSNMULTDSVRCU.PRIKXVLDLSNKKIKSVPKQVVKLEALOEN 479
 Db 413 NDENCSWPEITVVMNMLSTYKLSDSVRCLEKSIQIIDLNNQIQVTPKETIHLMAIRELN 472
 QY 480 VAFNSLITDLPGCCSFSSLSVLLIIDHNSVSPSADFPQSCOKMSISAGDNPFOCTCELR 539
 Db 473 IAFNFLTDLPGCSHPSRSLVLMENMFILSPSLDFQSCQEVITLNAGRPFCTCEKN 532
 QY 540 FVKNIIDQVSSEVLGMPDSYKCDYPESYRGSPPKDFHMSLSQNTILLIITIGATMLVLA 599
 Db 533 FIO-LETYSEVMMVGMDSYTCBPPLNLGRTRLKDVHLELSQNTALLIYTVIIVMLVLG 591
 QY 600 VTVTSLSCTIYLD.PWYLRMCOMTQTPRRARANPLELQRLLOPHAFISYSEHNSAWYKSE 659
 Db 592 LAVAPCCIAFDLPWYLRMGCCQTQWHRRKRTQEOELKRVRRHAFISYSEHSLWYKNE 651
 QY 660 LVPYLEKED--IOICLHERNPVPGKSIENVINIINCISEKSYKSIIVLSPNPFQSEWCHELY 717
 Db 652 LIPNLEKEKESGLICYESYFPDPKSISENIVESFIEKSYKSIIVLSPNPFQONMCHIEFY 711
 QY 718 FAHNHLFHEGSSNNLILILEPIPONSIPNKYHKLKALMTQRTYLOMPKEKSKGLFWANT 777
 Db 712 FAHNHLFHEHNSDHIILILEPIPFYCIPRYHKLKALLEKAYLEWPKDRRCKGLFWANL 771
 QY 778 RAAPFMKLTIVENNDDYKS 796
 Db 772 RAAINVNLATREMYELO 790
 US-09-992-598-57
 US-09-992-598-57
 / Sequence 57, Application US/09992598
 / Patent No. 6956108
 / GENERAL INFORMATION:
 / APPLICANT: Ashkenazi, Avi J.
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan L.
 / APPLICANT: Ferrara, Napoleone
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gerber, Hanspeter
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Guiney, Aiscin L.
 / APPLICANT: Kijavlin, Ivar J.
 / APPLICANT: Napier, Mary A.
 / APPLICANT: Pan, James
 / APPLICANT: Paoni, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Watanabe, Colin K.
 / APPLICANT: Williams, P. Mickey
 / APPLICANT: Wood, William I.
 / APPLICANT: Zhang, Zemin
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 / FILE REFERENCE: P2730PIC20

1	CURRENT APPLICATION NUMBER: 05/09/1992, 598
2	CURRENT FILING DATE: 2001-11-14
3	PRIOR APPLICATION NUMBER: 60/049787
4	PRIOR FILING DATE: 1997-06-16
5	PRIOR APPLICATION NUMBER: 60/062350
6	PRIOR FILING DATE: 1997-10-17
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71	PRIOR APPLICATION NUMBER: 60/088861
72	PRIOR FILING DATE: 1998-06-11
73	PRIOR APPLICATION NUMBER: 60/088876


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RESULT 9
US-09-989-735-57
; Sequence 57, Application US/09989735
; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bortstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC61
; CURRENT APPLICATION NUMBER: US/09/989,735
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC60
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 45.9%; Score 1905.5; DB 3; Length 811;
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Matches 382; Conservative 145; Mismatches 251; Indels 21; Gaps 10;

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QY 67 LOVSPMSLSBELTVARLSHNRQOLDLSVFEKNQOLEYVLDLSHNOLOKISCHPIVSFPHL 126
DB 63 LOSSDFHSVSKRLVILCHNRIOQLDLKTFEFNKELRYLDLSNNRKSVTWYLLAGLYL 122
QY 127 DLSFNDKALPICKKEFGNLSQNLFLGLSAMKLOKDLPLIAHLHSYILLDLRNYIKEN 186
DB 123 DLSFNDKALPICKKEFGNLSQNLFLGLSAMKLOKDLPLIAHLHSYILLDLRNYIKEN 180
QY 187 ETESQIINAKTLLHVFHPTSLFAIOVNI SVNTLQCLQLTNKLNDNCQVFIKLSBELT 246
DB 181 EESGPIINTYKTLHIVLPMDTFVWLIRDGIKTSKILEWTNI---DGKSGVSY--EQO 234
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DB 235 RNLSNENKTSVLLNKVDLMDLPLIIQFVWHTSVBHFQIRNVTFGKAYLDHNSFDY 294
QY 300 SKTTLKATLIEHTNQVFLFSQFALYTFVSENNIMLTISDTPFLHMLCPHASTFEKFLN 359
DB 295 SNTVWRTIKLEHVHRVFIYIOQDKIYLLTKNDINLTISNMQPHMLFPNPTFQOYN 354
QY 360 FTQNVFTDSIFPKSSTLVKLETLIIQKNGKDLFVYGLMTKMPSELEIIVDSWNSLESOR 419
DB 355 FANNILTDLEFKRTIQLPHLKTLLINGNKLFTLSVSCFANNTP--LEHIDLSQNLQH-K 412
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DB 413 NDENCSWETVNNMLSTNKLSDSVFRCLPKSIQIILDNNOIQVPEKTIHLMALREIN 472
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QY 540 FVKNIQVSEVLESGWPSYKCDYPSYRGSPKDFHNSLSCNTLLIVTIGATMLVIA 599
DB 533 FIQ-LETYSVWVMVMSDYTCYCEPLNLRGTRKDVHLHELSCNTALLIVTIVIMLVLG 591
QY 600 VTVYSLCIYLDLPWLRNVCQWOTQRRARRNIPLEIQLNLOPAFAISISEHDSAMVSE 659
DB 592 LAVARCCAHFDPWYLRMLGQCTQWHRVKTTOQLKKNVFFAHFISYSEHDSAMVXNE 651
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DB 772 RAALIVNVLATREMYELOT 790

RESULT 12
US-09-989-728-57
Sequence 57, Application US/09989728
Patent No. 7029873
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertschen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gutney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C72
CURRENT APPLICATION NUMBER: US/09/989,728
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/065186
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RESULT 13
US-09-997-349-57
; Sequence 57, Application US/09997349
; Patent No. 7034106
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerder, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guirney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C37
; CURRENT APPLICATION NUMBER: US/09/997,349
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; Patent No. 7034122
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlisen, Mary B.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, V. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC38
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; CURRENT FILING DATE: 2001-11-15
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APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
CURRENT FILING DATE: 2001-11-20
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13	777.2	28.2	3462	US-09-989-735-56	Sequence 56, App
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29	185.2	6.7	601	US-09-949-002-2393	Sequence 2393, App
30	185.2	6.7	601	US-09-949-002-9240	Sequence 9240, App
31	153.8	5.6	2351	US-09-949-016-2928	Sequence 2928, App
32	65.2	2.4	3347	US-09-954-987B-169	Sequence 169, App
33	65.2	2.4	3347	US-09-954-987B-168	Sequence 168, App
34	63.6	2.3	3150	US-09-954-987B-174	Sequence 174, App
35	63.6	2.3	3243	US-09-954-987B-173	Sequence 173, App
36	63.6	2.3	3283	US-09-999-833A-495	Sequence 495, App
37	63.6	2.3	3283	US-10-020-445A-495	Sequence 495, App
38	63.6	2.3	3283	US-09-978-189-495	Sequence 495, App
39	63.6	2.3	3283	US-10-017-085A-495	Sequence 495, App
40	63.6	2.3	3283	US-10-145-128A-495	Sequence 495, App
41	63.6	2.3	3283	US-10-013-928A-495	Sequence 495, App
42	63.6	2.3	3283	US-10-013-917A-495	Sequence 495, App
43	61.2	2.2	3096	US-09-954-987B-191	Sequence 191, App
44	61.2	2.2	3220	US-09-954-987B-190	Sequence 190, App
45	56.6	2.1	1141	US-09-806-708B-22	Sequence 22, App

ALIGNMENTS

RESULT 1
US-09-949-002-226
; Sequence 226, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 226
; LENGTH: 2758
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-226

Query Match	99.9%	Score 2749.8	DB 3	Length 2758
Best Local Similarity	99.9%	Pred. No. 0		
Matches 2751	Conservative	0	Mismatches 2	Indels 0
			Gaps 0	
QY	1	AGAAATTTGACATCATATCAAGATGCTTGAAGAGAACACCCCTTAGATGACACTGC	60	
DB	2	AGAAATTTGACATCATATCAAGATGCTTGAAGAGAACACCCCTTAGATGACACTGC	61	
QY	61	AAACATCATGACCAAGACCAAGACCTTATTTAAAGCTTCCATTTTGTTCCTTATG	120	
DB	62	AAACATCATGACCAAGACCAAGACCTTATTTAAAGCTTCCATTTTGTTCCTTATG	121	
QY	121	ATCATTAATAGTTGGAACCAAGATCCAGTTCTCCGACGGAATGATTTGACATAGACAG	180	
DB	122	ATCATTAATAGTTGGAACCAAGATCCAGTTCTCCGACGGAATGATTTGACATAGACAG	181	
QY	181	TCAAAAAGAGGCTTATTCATGTTTCAAAAGCTTACCGCTGAAAAACCAAGTCTTAAAT	240	
DB	182	TCAAAAAGAGGCTTATTCATGTTTCAAAAGCTTACCGCTGAAAAACCAAGTCTTAAAT	241	
QY	241	ATGTTCTGAACTCATATGCTGAGCTTCAAGCTTCTGACATGAGCTTCTATCAAGTTG	300	
DB	242	ATGTTCTGAACTCATATGCTGAGCTTCAAGCTTCTGACATGAGCTTCTATCAAGTTG	301	

QY 301 ACAGTTTGAGACTTCCCATAAACAGAACTCAGCTACCTGATTTAAAGTGTTCAGATTC 360
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Db 302 ACAGTTTGAGACTTCCCATAAACAGAACTCAGCTACCTGATTTAAAGTGTTCAGATTC 361
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QY 361 AACCGAGATTGAAATATTGAAATTTATCTCATTAATCACTGCAAAAGATATCTGGCCAT 420
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Db 362 AACCGAGATTGAAATATTGAAATTTATCTCATTAATCACTGCAAAAGATATCTGGCCAT 421
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QY 421 CCTATTGTGAGTTTCAGGCAATTTAGATCTCTCATTCATGATTTTCAAGGCCCTGCCCATC 480
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Db 422 CCTATTGTGAGTTTCAGGCAATTTAGATCTCTCATTCATGATTTTCAAGGCCCTGCCCATC 481
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QY 481 TGTAAAGAAATTTGGCACTTATCAACAAGTATTTCTGGAGTTGAGTGTCTATGAAGCTG 540
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Db 482 TGTAAAGAAATTTGGCAACTTATCAACAAGTATTTCTGGAGTTGAGTGTCTATGAAGCTG 541
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QY 541 CAAAAATTGAAATTTGCTGCAATTTGCTCACTTGCATCTTAAGTTATTCCTTCTGCAATTTA 600
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Db 542 CAAAAATTGAAATTTGCTGCAATTTGCTCACTTGCATCTTAAGTTATTCCTTCTGCAATTTA 601
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Db 602 AGAAATTTATATATAAAAGAAATGAGACAGAAAGTCTACAAATTTCTGAATGCAGAAAAC 661
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Db 662 CTTCACCTTGTTCACCCCACTAGTTTATTCGCTATCCAAAGTGAAACATATCAGTTAAT 721
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QY 721 ACTTTAGGGTGCTTCAACGTGACTAATTTAAATGGAATGAGCAACGTCAAGTTTC 780
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Db 722 ACTTTAGGGTGCTTCAACGTGACTAATTTAAATGGAATGAGCAACGTCAAGTTTC 781
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QY 781 ATTTAAATTTTATCAGAACTCACAGAGGTTCAACCTTACGTGAATTTTACCTCAACAC 840
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Db 782 ATTTAAATTTTATCAGAACTCACAGAGGTTCAACCTTACGTGAATTTTACCTCAACAC 841
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QY 841 ATGAAAGCACTTGGAAATGCTGCTGCTCAGAGTCTTCAAATTTCTTGCCCAACCTGTG 900
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Db 842 ATGAAAGCACTTGGAAATGCTGCTGCTCAGAGTCTTCAAATTTCTTGCCCAACCTGTG 901
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QY 901 GAAATATCTCAATTAATTTACAAATTTTAAATTTGAAAGCAATTCGTGAAGAAATTTTACT 960
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Db 902 GAAATATCTCAATTAATTTACAAATTTTAAATTTGAAAGCAATTCGTGAAGAAATTTTACT 961
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QY 961 TATTTCAAAACGACATTTGAAACATTTGACATTAAGAAATATCAACGAACCAAGTTTCTG 1020
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QY 1021 TTTTCAACGACAGCTTTGTACACCGTGTTCCTGAGATGAACATTAATGATTTAACCAT 1080
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QY 1081 TCAGATTAACCTTTTATACACATGCTGCTGCTCAGATGCAACGAACATTTCAAGTTTTCG 1140
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Db 1082 TCAGATTAACCTTTTATACACATGCTGCTGCTCAGATGCAACGAACATTTCAAGTTTTCG 1141
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QY 1141 AACTTTACCCGAAACGTTTTCACAGATAGTATTTTGAAGAAATGTTCCACGTTAGTTAA 1200
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Db 1142 AACTTTACCCGAAACGTTTTCACAGATAGTATTTTGAAGAAATGTTCCACGTTAGTTAA 1201
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QY 1201 TTGAGACACTTATCTTCAAAAAATGATTTAAAGACCTTTTCAAGATGCTCATG 1260
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Db 1202 TTGAGACACTTATCTTCAAAAAATGATTTAAAGACCTTTTCAAGATGCTCATG 1261
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QY 1261 ACGAAGGATATGCTCTTCTTGAAGAAATCGAGATTTAGCTGGAATCTTTGGAATCTGAT 1320
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Db 1262 ACGAAGGATATGCTCTTCTTGAAGAAATCGAGATTTAGCTGGAATCTTTGGAATCTGAT 1321
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QY 1321 AGACATTAAGAAAGACGCTTGGGTTGAGAGTATGAGTGTGTTAAATTTGCTTCAAT 1380
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Db 1322 AGACATTAAGAAAGACGCTTGGGTTGAGAGTATGAGTGTGTTAAATTTGCTTCAAT 1381
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QY 1381 ATGCTTACTGACTCTGTTCAGATGTTTAACTCCAGGATCAAGGTAAGTATCTTCAAC 1440
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Db 1382 ATGCTTACTGACTCTGTTCAGATGTTTACTCTCCAGAGATCAAGGTACTGATTTCAAC 1441
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QY 1441 AGCAATTAAGAAAGGCTTCTTAAACAAGTCGTAAACCTGGAAGCTTTGCAAGAACTC 1500
| | | | |
Db 1442 AGCAATTAAGAAAGGCTTCTTAAACAAGTCGTAAACCTGGAAGCTTTGCAAGAACTC 1501
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QY 1501 AATGTGCTTTCATATCTTTTAACTGACCTTCTGAGTGTGCAAGCTTTTACAGACCTTTCT 1560
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Db 1502 AATGTGCTTTCATATCTTTTAACTGACCTTCTGAGTGTGCAAGCTTTTACAGACCTTTCT 1561
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Db 1562 GATTTGATCATTTGATCAAAATTCAGTTTCCACCCATGGGCGATTTCTTCAGAGCTGCG 1621
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QY 1621 CAGAGATGAGGTCATATAAGCAGAGGAGCAATTCATTCCAATGTACCTGTGAGCTAAGA 1680
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Db 1622 CAGAGATGAGGTCATATAAGCAGAGGAGCAATTCATTCCAATGTACCTGTGAGCTAAGA 1681
| | | | |
QY 1681 GAATTTGTCAAAAAATATAGACCAAGTATCAAGTGAAGTGTAGAGGCTGGCTGATTTCT 1740
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Db 1682 GAATTTGTCAAAAAATATAGACCAAGTATCAAGTGAAGTGTAGAGGCTGGCTGATTTCT 1741
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QY 1741 TATTAAGTGACTACCCGAAAGTTATAGAGAAACCCACCTTAAGSACTTTTCACTGCTCT 1800
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Db 1742 TATTAAGTGACTACCCGAAAGTTATAGAGAAACCCACCTTAAGSACTTTTCACTGCTCT 1801
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QY 1801 GAATTAATCCGCAACATTAATCTGTGATGCTGACATCTGGTGCCACCATGCTGTGTG 1860
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Db 1802 GAATTAATCTGCAACATTAATCTGTGATGCTGACATCTGGTGCCACCATGCTGTGTG 1861
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QY 1861 GCTGTGACTGTGACCTCCCTCTGCAATCTTGAATCTGCTGCTGATCTCAGATGCTG 1920
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Db 1862 GCTGTGACTGTGACCTCCCTCTGCAATCTTGAATCTGCTGCTGATCTCAGATGCTG 1921
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QY 1921 TGCCAGTGAACCCCAACCTCGGCGAGGCGCAGGAACATACCTTTGAAGAACTCCAAAGA 1980
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Db 1922 TGCCAGTGAACCCCAACCTCGGCGAGGCGCAGGAACATACCTTTGAAGAACTCCAAAGA 1981
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QY 1981 AACCTCAAGTTTCATGCTTTTATTTCAATATGTAAGAACTGATTCGCTGGGTGAAAAAGT 2040
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Db 1982 AACCTCAAGTTTCATGCTTTTATTTTCAATATGTAAGAACTGATTCGCTGGGTGAAAAAGT 2041
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QY 2041 GAATTTGTAACCTTACTAGAAAAAGAAATATACAGATTTGTCTTCATGAGAGAACTTT 2100
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QY 2101 GTCCCTGGCAAGAGATTTGTGAAATATATCATCACTGCAATTTGANAAGATTAACAAGTCC 2160
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Db 2102 GTCCCTGGCAAGAGATTTGTGAAATATATCATCACTGCAATTTGANAAGATTAACAAGTCC 2161
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QY 2161 ATCTTTGTTTGTCTCCCAACTTTGTCCAGAGTGAAGTGTGCAATTAAGAACTCATTTT 2220
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Db 2162 ATCTTTGTTTGTCTCCCAACTTTGTCCAGAGTGAAGTGTGCAATTAAGAACTCATTTT 2221
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QY 2221 GCCCATCACAATCTTTTCATGAAAGATCTATAAATTAATCTCATCTTACTGGAACCC 2280
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Db 2222 GCCCATCACAATCTTTTCATGAAAGATCTATAAATTAATCTCATCTTACTGGAACCC 2281
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QY 2281 ATTTCAACGAAACAGATTTCCCAACAGTACCAACAGCTGGAAGCTCTATGACGACGGG 2340
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Db 2282 ATTTCAACGAAACAGATTTCCCAACAGTACCAACAGCTGGAAGCTCTATGACGACGGG 2341
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QY 2341 ACTTAATTTGCAAGTGGCCCAAGGAGAAAGCAACGTTGGGCTTCTTTGGGCTTAACATTAGA 2400
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Db 2342 ACTTAATTTGCAAGTGGCCCAAGGAGAAAGCAACGTTGGGCTTCTTTGGGCTTAACATTAGA 2401
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QY 2401 GCGGCTTTTATATGAAATTTAACTAGTCACTGAAAAAATGATGTGAATCTTAAATA 2460
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Db 2402 GCGGCTTTTATATGAAATTTAACTAGTCACTGAAAAAATGATGTGAATCTTAAATA 2461
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QY 2461 AATTTAGAAATTTCACTTAAGAAACATTAATTTCTTGAATGATGTGAATGTAGACGT 2520
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Db 2462 AATTAGAAATTCACCTTAAGAAACCATTAATTAATTGATGATGATGATAGTACAGT 2521
Qy 2521 CGTAAGTAACTGCTGGAGAGTGCTCCATTAATCCATGCTTCAGGAAGAAGCTTAACA 2580
Db 2522 CTTAAGTAACTGCTGGAGAGTGCTCCATTAATCCATGCTTCAGGAAGAAGCTTAACA 2581
Qy 2581 AACAATATTTTCATCTGGGAACTGAGCTAGCGGCTGAGGTTAGCTGCGCAGTTAGAGAC 2640
Db 2582 AACAATATTTTCATCTGGGAACTGAGCTAGCGGCTGAGGTTAGCTGCGCAGTTAGAGAC 2641
Qy 2641 AGCCAGTCTCTTCTGCTTTAATCATTAATGTTCAAAATGAAACAGTCTCTTTGAGTAA 2700
Db 2642 AGCCAGTCTCTTCTGCTTTAATCATTAATGTTCAAAATGAAACAGTCTCTTTGAGTAA 2701
Qy 2701 ATGCTAGTTTTCAGCTCTCTCCAGCTGCTTCCCAATGATGATCTGTTG 2753
Db 2702 ATGCTAGTTTTCAGCTCTCTCCAGCTGCTTCCCAATGATGATCTGTTG 2754

RESULT 2

US-09-949-002-672
; Sequence 672, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 672
; LENGTH: 6758
; TYPE: DNA
; ORGANISM: Human
; US-09-949-002-672

Query Match 99.9%; Score 2749.8; DB 3; Length 6758;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGAATTTGACTCATATCAAGATGCTCTGAGAAGAACCACTTTAGGATAGCACTGC 60
Db 2002 AGAATTTGACTCATATCAAGATGCTCTGAGAAGAACCACTTTAGGATAGCACTGC 2061
Qy 61 AACATCAGACCAAGACAAAGAACCTATTTGTTAAAAGCTTCCATTTTGTTCCTTATG 120
Db 2062 AACATCAGACCAAGACAAAGAACCTATTTGTTAAAAGCTTCCATTTTGTTCCTTATG 2121
Qy 121 ATCATATATGTTGGAACAGAACTCAGTCTCCGACGGAATGAATTTGCAATAGACAAG 180
Db 2122 ATCATATATGTTGGAACAGAACTCAGTCTCCGACGGAATGAATTTGCAATAGACAAG 2181
Qy 181 TCAAAAAGAGTCTTATTCATGTTCCAAAAGACCTACCGCTGAAAAACAAAGCTTTAGAT 240
Db 2182 TCAAAAAGAGTCTTATTCATGTTCCAAAAGACCTACCGCTGAAAAACAAAGCTTTAGAT 2241
Qy 241 ATGCTCAGAACTAATGCTGAGCTTCAAGTCTCTGACATAGAGCTTTCTATCAAGTTG 300
Db 2242 ATGCTCAGAACTAATGCTGAGCTTCAAGTCTCTGACATAGAGCTTTCTATCAAGTTG 2301
Qy 301 ACAGTTTGAAGCTTTCCCATTAACAGAACTCAGCTACTGATTGAAGTCTTCAAGTTC 360
Db 2302 ACAGTTTGAAGCTTTCCCATTAACAGAACTCAGCTACTGATTGAAGTCTTCAAGTTC 2361
Qy 361 AACCGATTTTGAATATTTGGATTTATCTCAATCAGTTGCAAAAAGATATCTGCCAT 420
Db 2362 AACCGATTTTGAATATTTGGATTTATCTCAATCAGTTGCAAAAAGATATCTGCCAT 2421

Qy 421 CCTATTTGAGTTTCAGGACATTTAGATCTCTCAATCAATGATTTCAAGGCCCTGCCATC 480
Db 2422 CCTATTTGAGTTTCAGGACATTTAGATCTCTCAATCAATGATTTCAAGGCCCTGCCATC 2481
Qy 481 TGTAAAGAAATTTGSCAATTTATCACTGAATTTCTTGGAGTGAAGTCTATGAAGCTG 540
Db 2482 TGTAAAGAAATTTGSCAATTTATCACTGAATTTCTTGGAGTGAAGTCTATGAAGCTG 2541
Qy 541 CAAAAATTAAGATTTGCTGCCAATTTGCTCACTTGCATTAAGTATATCTTGTGATTTA 600
Db 2542 CAAAAATTAAGATTTGCTGCCAATTTGCTCACTTGCATTAAGTATATCTTGTGATTTA 2601
Qy 601 AGAAATTTATATATAAAGAAATAGACAGAAAGTCTACAATTTCTGAATGCAAAAAAC 660
Db 2602 AGAAATTTATATATAAAGAAATAGACAGAAAGTCTACAATTTCTGAATGCAAAAAAC 2661
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Db 2662 CTTCACCTGTTTTTCAACCAACTAGTTATTCGATATCCAAAGTGAACATACATTAAT 2721
Qy 721 ACTTAAGGCTGCTTCAACTGACTAATTAATTTGAATGATGACAACTGTCAAGTTTC 780
Db 2722 ACTTAAGGCTGCTTCAACTGACTAATTAATTTGAATGATGACAACTGTCAAGTTTC 2781
Qy 781 ATTAATTTTATATGAACTGACCTGAGGTTCAACCTTACTGAATTTTACCCTCAACAC 840
Db 2782 ATTAATTTTATATGAACTGACCTGAGGTTCAACCTTACTGAATTTTACCCTCAACAC 2841
Qy 841 ATGAAACGACTTGGAAATGCTGTGCTGAGAGTCTTCAATTTCTTTGGCCCAACCTGTG 900
Db 2842 ATGAAACGACTTGGAAATGCTGTGCTGAGAGTCTTCAATTTCTTTGGCCCAACCTGTG 2901
Qy 901 GAATATCTCAATTTTAACTTAATTTAACTAATTTGAAGATTTGCGAAGAAATTTTACT 960
Db 2902 GAATATCTCAATTTTAACTTAATTTAACTAATTTGAAGATTTGCGAAGAAATTTTACT 2961
Qy 961 TATTTAAACGACATTTGAAGCATTTGACATTAAGAACATATGACGAACTAAGTTTCTG 1020
Db 2962 TATTTAAACGACATTTGAAGCATTTGACATTAAGAACATATGACGAACTAAGTTTCTG 3021
Qy 1021 TTTTCACAGACAGCTTTGTACACCGTGTCTTCTGAGATGAACTATTGATGTTAACAT 1080
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Qy 1081 TCAGATACACCTTTTATACATGCTGTGCTCTACGACCAAGCACTTCAAGTTTGTG 1140
Db 3082 TCAGATACACCTTTTATACATGCTGTGCTCTACGACCAAGCACTTCAAGTTTGTG 3141
Qy 1141 AACTTACCAGAACGTTTTCACAGATGATTTTGAAGAAATGTTCCACGTTAGTTAA 1200
Db 3142 AACTTACCAGAACGTTTTCACAGATGATTTTGAAGAAATGTTCCACGTTAGTTAA 3201
Qy 1201 TTGAGACACTTATCTTCAAAAAATGATTTAAAGACCTTTTCAAGATGAGTCTCATG 1260
Db 3202 TTGAGACACTTATCTTCAAAAAATGATTTAAAGACCTTTTCAAGATGAGTCTCATG 3261
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Db 3262 ACGAAGATATGCTTTCTTGAAGATCTGAATGTTTACCTCCAGAGATCAAGTTACTTTCAC 3321
Qy 1321 AGACATTAAGAAACCTGACCTTGGTGAAGATATAGAGGTATTAATTTGTCTCAAT 1380
Db 3322 AGACATTAAGAAACCTGACCTTGGTGAAGATATAGAGGTATTAATTTGTCTCAAT 3381
Qy 1381 ATGCTTACGACTGTTTTGAGATGTTTACCTCCAGAGATCAAGTTACTTTCAC 1440
Db 3382 ATGCTTACGACTGTTTTGAGATGTTTACCTCCAGAGATCAAGTTACTTTCAC 3441
Qy 1441 AGCAATTAATAAGAGGCTTCTTAACAAGTCTTAATAAGCTTGAAGAACTGCAAGAACTC 1500
Db 3442 AGCAATTAATAAGAGGCTTCTTAACAAGTCTTAATAAGCTTGAAGAACTGCAAGAACTC 3501
Qy 1501 AATGTTGCTTCAATTTCTTAAGTGAAGTCTGAGATGAGCAAGCTTGAAGAGCTTCT 1560

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Db 3502 AATGTTGCTTCAATCTTTAACTGACCTTCTGGATGTGGAGCTTTAGACCTTTCT 3561
Oy 1561 GTATTGATCATGTGACAAATTCAGTTTCCACCCATGGCGATTTCTTCCAGAGCTGC 1620
Db 3562 GTATTGATCATGTGACAAATTCAGTTTCCACCCATGGCGATTTCTTCCAGAGCTGC 3621
Oy 1621 CAGAAGATGAGTCAATTAAGCAGGAGCAATCCATTCATTCAGTATCCTGTAGCTAAGA 1680
Db 3622 CAGAAGATGAGTCAATTAAGCAGGAGCAATTCATTCAGTATCCTGTAGCTAAGA 3681
Oy 1681 GAATTTGTCAAAAATATAGACCAAGTATCAAGTAAAGTGTAGAGGCTGCGCTTAATCT 1740
Db 3682 GAATTTGTCAAAAATATAGACCAAGTATCAAGTAAAGTGTAGAGGCTGCGCTTAATCT 3741
Oy 1741 TATAAGTGATACCCAGAAAGTTATAGAGAGCCCACTAAGGACTTTTCAATGTCT 1800
Db 3742 TATAAGTGATACCCAGAAAGTTATAGAGAGCCCACTAAGGACTTTTCAATGTCT 3801
Oy 1801 GAATTAATCCTGCAACATAAATCTGCTGATCGTCAACATCGGTGCCACATGCTGTGTG 1860
Db 3802 GAATTAATCCTGCAACATAAATCTGCTGATCGTCAACATCGGTGCCACATGCTGTGTG 3861
Oy 1861 GCTGTGACTGTGACCTCCCTCTGCAATCTAATTTGATCTGCTGCTGTATCTCAGATGTG 1920
Db 3862 GCTGTGACTGTGACCTCCCTCTGCAATCTAATTTGATCTGCTGCTGTATCTCAGATGTG 3921
Oy 1921 TGCCAGTGGACCCCAACTCGGGCAGGGCCAGGAACATCCCTTGAAACATCCCAAGA 1980
Db 3922 TGCCAGTGGACCCCAACTCGGGCAGGGCCAGGAACATCCCTTGAAACATCCCAAGA 3981
Oy 1981 AACCTCCAGTTTCATGCTTTTATTTCAATAGTGAACATGTTGCTGCTGTGAAGT 2040
Db 3982 AACCTCCAGTTTCATGCTTTTATTTCAATAGTGAACATGTTGCTGCTGTGAAGT 4041
Oy 2041 GAATTTGTATCCTTACCTAGAAAAAGAAATATACAGATTTGCTTTCATGAGAACTTT 2100
Db 4042 GAATTTGTATCCTTACCTAGAAAAAGAAATATACAGATTTGCTTTCATGAGAACTTT 4101
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Db 4102 GTCCTGGAGAAAGATGTGGAAAAATATCATCACTGATGAGAAGTTTACAAGTCC 4161
Oy 2161 ATCTTTGTTTTGTCTCCAACTTTGTCAGAGTGAAGTGGCATTCAGAACTTATTTT 2220
Db 4162 ATCTTTGTTTTGTCTCCAACTTTGTCAGAGTGAAGTGGCATTCAGAACTTATTTT 4221
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Db 4222 GCCCATCACATCTCTTTCATAGAGATCTTAATTAATCTCATCTTACTGGAACCC 4281
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Db 4282 ATTCACAGAAAGATTCCTCCAAAGTACCAAGCTGAAGCTCTCAAGCGAGCG 4341
Oy 2341 ACTTATTTGCAAGTGGCCCAAGAGAAACAAAGCTGCTTTTGAGCTTAACATTAGA 2400
Db 4342 ACTTATTTGCAAGTGGCCCAAGAGAAACAAAGCTGCTTTTGAGCTTAACATTAGA 4401
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Db 4402 GCCGCTTTTAAATATGAAATTTAACTAGTCACTGAAAACATGATGTGAATCTTAAAA 4461
Oy 2461 AATTAGAGAAATTCACCTTAAGAAACATTAATTTACTTGGATGATGTGAATAGTACAT 2520
Db 4462 AATTAGAGAAATTCACCTTAAGAAACATTAATTTACTTGGATGATGTGAATAGTACAT 4521
Oy 2521 CGTAAGTAACTGTCTGAGAGTGTCTCATTTCTCATGCTTCAGAGAAAGACTTAACA 2580
Db 4522 CGTAAGTAACTGTCTGAGAGTGTCTCATTTCTCATGCTTCAGAGAAAGACTTAACA 4581
Oy 2581 AAAACAATGTTTCATCTGGGAACTGAGCTAGGCGGTAGGCTTACCTGCAAGTTAGAGAC 2640
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Db 4582 AAAACAATGTTTCATCTGGGAACTGAGCTAGGCGGTAGGCTTACCTGCAAGTTAGAGAC 4641
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Db 4642 AGCCAGTCTCTCTGTTTAACTATGTTTCAAAATTTGAAGAGTCTTTTGAAGTAA 4701
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RESULT 3
US-09-949-002-798
; Sequence 798, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 798
; LENGTH: 6758
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-798

Query Match 99.9%; Score 2749.8; DB 3; Length 6758;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 2; Indels 0; Gaps 0;

Matches 2751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Oy 1 AGAATTTGACTCATATCAAGATGCTTGAAGAAACAAACCTTTAGATAGCCACTGC 60
Db 2002 AGAATTTGACTCATATCAAGATGCTTGAAGAAACAAACCTTTAGATAGCCACTGC 2061
Oy 61 AACATCATGACCAAGAAAGAAACCTATTTGTTAAAGCTTCCATTTTGGCTTATG 120
Db 2062 AACATCATGACCAAGAAAGAAACCTATTTGTTAAAGCTTCCATTTTGGCTTATG 2121
Oy 121 ATCATTAATAGTTGAACAGAAATCCAGTTCCTCGACGAAATGAATTCAGTAGACAAG 180
Db 2122 ATCATTAATAGTTGAACAGAAATCCAGTTCCTCGACGAAATGAATTCAGTAGACAAG 2181
Oy 181 TCAAAAAGAGTCTTATTCATGTTCCAAAAGACCTACCGCTGAACCAAAAGCTTAGAT 240
Db 2182 TCAAAAAGAGTCTTATTCATGTTCCAAAAGACCTACCGCTGAACCAAAAGCTTAGAT 2241
Oy 241 ATGTCTCAAGATACATGCTGAGTCTGAGTCTCTGACATGAGTCTTCTATCAGAGTTG 300
Db 2242 ATGTCTCAAGATACATGCTGAGTCTGAGTCTCTGACATGAGTCTTCTATCAGAGTTG 2301
Oy 301 ACAGTTTGAAGCTTCCCATTAACAAGATCCAGCTACTGATTTAAGTTTTCAGTTTC 360
Db 2302 ACAGTTTGAAGCTTCCCATTAACAAGATCCAGCTACTGATTTAAGTTTTCAGTTTC 2361
Oy 361 AACAGAGATTTAGATATTTGATTTATCTCATATCAGTTGCAAAAGATATCTGCCAT 420
Db 2362 AACAGAGATTTAGATATTTGATTTATCTCATATCAGTTGCAAAAGATATCTGCCAT 2421
Oy 421 CCTATTTGAGTTTCAGGCAATTTAGATCTCTCATTAATTAAGATTTTCAGGCTTCCATC 480
Db 2422 CCTATTTGAGTTTCAGGCAATTTAGATCTCTCATTAATTAAGATTTTCAGGCTTCCATC 2481
Oy 481 TGTAGGAATTTGGAACTTATCAACTGAATTTCTTGGAGTTGAGTGTATGAAGCTG 540
Db 2482 TGTAGGAATTTGGAACTTATCAACTGAATTTCTTGGAGTTGAGTGTATGAAGCTG 2541
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541 CAAAAATGATGTCGCAATGCTCATCTGACCTAAGTTAATCTCTGATTTA 600
Db CAAAAATGATGTCGCAATGCTCATCTGACCTAAGTTAATCTCTGATTTA 2601
Qy AGAAATTTATATATAAGAAAATGACAGAAAGCTTCAAAATCTGATGCCAAAAC 660
Db AGAAATTTATATATAAGAAAATGACAGAAAGCTTCAAAATCTGATGCCAAAAC 2661
Qy CTGACCTGTTTTCACCCCACTAGTTATTCGATATCAAGTCAAGTATCAGTTAT 720
Db CTGACCTGTTTTCACCCCACTAGTTATTCGATATCAAGTCAAGTATCAGTTAT 2721
Qy ACTTTAGGGTGCTTCAACTGACTAATATTAATGATGACAACTGTCAGATTTTC 780
Db ACTTTAGGGTGCTTCAACTGACTAATATTAATGATGACAACTGTCAGATTTTC 2781
Qy ATTAATTTTATATGAAACTCACAGAGGTTCAACTTATGAAATTTTACCTCAACAC 840
Db ATTAATTTTATATGAAACTCACAGAGGTTCAACTTATGAAATTTTACCTCAACAC 2841
Qy ATAGAAAGCACTTGAAGAAAGCTGTCAGAGTCTTCAATTTCTTTGGCCCAACCTGG 900
Db ATAGAAAGCACTTGAAGAAAGCTGTCAGAGTCTTCAATTTCTTTGGCCCAACCTGG 2901
Qy GAATATCTCAATATTTTCAATTTTAACTAATTTGAAGATTCGTGAGAGATTTTACT 960
Db GAATATCTCAATATTTTCAATTTTAACTAATTTGAAGATTCGTGAGAGATTTTACT 2961
Qy TATTTCTAAAACGACATTTGAAGCATTTGACATATGAAACCAAGTCTTTCTG 1020
Db TATTTCTAAAACGACATTTGAAGCATTTGACATATGAAACCAAGTCTTTCTG 3021
Qy TTTTTCACAGACGCTTTGACACCGTGTCTGAGATGACATTTATGATTTAACCAT 1080
Db TTTTTCACAGACGCTTTGACACCGTGTCTGAGATGACATTTATGATTTAACCAT 3081
Qy TCAGATACACCTTTTATACACATGCTGTCTGATGACCAAGACATTTCAAGTTTTC 1140
Db TCAGATACACCTTTTATACACATGCTGTCTGATGACCAAGACATTTCAAGTTTTC 3141
Qy AACCTTACCCAGAACGTTTTTCACAGATGATTTTGGAAAATGTTCCAGTTAGTTAA 1200
Db AACCTTACCCAGAACGTTTTTCACAGATGATTTTGGAAAATGTTCCAGTTAGTTAA 3201
Qy TTTGAGACACTTATCTTACAAAAAATGATTTAAAGACCTTTTCAAGTACGTCATG 1260
Db TTTGAGACACTTATCTTACAAAAAATGATTTAAAGACCTTTTCAAGTACGTCATG 3261
Qy AGAAGATATGCTCTTTGGAATFACGATGTTAGCTGGAATTTCTTGGATCTGGT 1320
Db AGAAGATATGCTCTTTGGAATFACGATGTTAGCTGGAATTTCTTGGATCTGGT 3321
Qy AGACATTAAGAAAACCTGACCTTGGGTGAGATATAGTGCTTAAATTTGCTTCAAT 1380
Db AGACATTAAGAAAACCTGACCTTGGGTGAGATATAGTGCTTAAATTTGCTTCAAT 3381
Qy ATGCTTACTGACTCTGTTTTGAGATGTTTACTCCAGAGATCAAGGTACTGATCTTAC 1440
Db ATGCTTACTGACTCTGTTTTGAGATGTTTACTCCAGAGATCAAGGTACTGATCTTAC 3441
Qy AGCAATTAATAATTAAGAGGCTCTTAACCAAGTGTAAACCTGAAGCTTTGCAAGAC 1500
Db AGCAATTAATAATTAAGAGGCTCTTAACCAAGTGTAAACCTGAAGCTTTGCAAGAC 3501
Qy AATGTTGCTTCAATTTCTTAACTGACCTTCTGAGTGTGGAGCTTTAGCAGCTTTCT 1560
Db AATGTTGCTTCAATTTCTTAACTGACCTTCTGAGTGTGGAGCTTTAGCAGCTTTCT 3561
Qy GTATTGATCATTTGATCAAAATTCAGTTTCCCAACCATCGGCTGATTTTCTCAGAGCTGC 1620
Db GTATTGATCATTTGATCAAAATTCAGTTTCCCAACCATCGGCTGATTTTCTCAGAGCTGC 3621
Qy CAGAAGATGAGTCAATAAAGCAGGGGACATTCATTCATGTATGCTGAGCTAAGA 1680

3622 CAGAAGATGAGTCAATAAAGCAGGGGACATTCATTCATGTATGCTGAGCTAAGA 3681
Qy GAAATTTGCAAAAATATATGACCAAGATATCAAGTAAAGTTTATGAGGCTGCTCATTC 1740
Db GAAATTTGCAAAAATATATGACCAAGATATCAAGTAAAGTTTATGAGGCTGCTCATTC 3741
Qy TATATGAGTACATCCAGAAAAGTATATAGAGAACCCACTTAAGAGACTTTTACATGCT 1800
Db TATATGAGTACATCCAGAAAAGTATATAGAGAACCCACTTAAGAGACTTTTACATGCT 3801
Qy GAATATATCTGCAACATTAATCTGCTGATTCGTCACCATTCGAGTCCACCATGCTGCTG 1860
Db GAATATATCTGCAACATTAATCTGCTGATTCGTCACCATTCGAGTCCACCATGCTGCTG 3861
Qy GCTGTGACTGTGACCTCCCTCTGCAATCTTATGATTCATCTGCTGCTGATTCAGATGCTG 1920
Db GCTGTGACTGTGACCTCCCTCTGCAATCTTATGATTCATCTGCTGCTGATTCAGATGCTG 3921
Qy TGCCAGTGAACCCAGACTCGGCGCAGGGCAGGAACATACCTTGAAGAACTCCAAAGA 1980
Db TGCCAGTGAACCCAGACTCGGCGCAGGGCAGGAACATACCTTGAAGAACTCCAAAGA 3981
Qy AACCTTCAGTTTCATGCTTTTATTTTATATATGTAAGATGATTCGCTGAGTGAAGT 2040
Db AACCTTCAGTTTCATGCTTTTATTTTATATATGTAAGATGATTCGCTGAGTGAAGT 4041
Qy GAATTTGTAACCTTACCTTGAAGAAAAGATATACAGATTTTGTCTTATGAGAACTTT 2100
Db GAATTTGTAACCTTACCTTGAAGAAAAGATATACAGATTTTGTCTTATGAGAACTTT 4101
Qy GTTCCGCAAGAGATGTAAGAAATATATCAATGCAATGCAATGTAAGAGTTTCAAGTCC 2160
Db GTTCCGCAAGAGATGTAAGAAATATATCAATGCAATGCAATGTAAGAGTTTCAAGTCC 4161
Qy GTTCCGCAAGAGATGTAAGAAATATATCAATGCAATGCAATGTAAGAGTTTCAAGTCC 4221
Db GTTCCGCAAGAGATGTAAGAAATATATCAATGCAATGCAATGTAAGAGTTTCAAGTCC 4281
Qy GCCCATCAAAATCTCTTATGTAAGAGATCTAATAATCTTATCTCATCTTATGTAAGCC 2280
Db GCCCATCAAAATCTCTTATGTAAGAGATCTAATAATCTTATCTCATCTTATGTAAGCC 4281
Qy ATTCACAGAACAGATTCACCAAGATGTAAGAGATGTAAGAGATGTAAGAGATGTAAG 2340
Db ATTCACAGAACAGATTCACCAAGATGTAAGAGATGTAAGAGATGTAAGAGATGTAAG 4341
Qy ACTTATTTGCAAGTGCCTCAAGAGAAAGCAAACTGAGGCTTTTGGGCTTAACTTAA 2400
Db ACTTATTTGCAAGTGCCTCAAGAGAAAGCAAACTGAGGCTTTTGGGCTTAACTTAA 4401
Qy GCCGCTTTTATATGTAAGATTAACACTAGTCACTGAAAAATGATGTAAGATCTTAA 2460
Db GCCGCTTTTATATGTAAGATTAACACTAGTCACTGAAAAATGATGTAAGATCTTAA 4461
Qy AATTTAGGAATTTCACTTAAGAAACCATTTATTTACTGATGATGTAAGATGTAAG 2520
Db AATTTAGGAATTTCACTTAAGAAACCATTTATTTACTGATGATGTAAGATGTAAG 4521
Qy AATTTAGGAATTTCACTTAAGAAACCATTTATTTACTGATGATGTAAGATGTAAG 2580
Db AATTTAGGAATTTCACTTAAGAAACCATTTATTTACTGATGATGTAAGATGTAAG 4581
Qy CGTAACTAGTCTGAGAGTGCCTCAATTTTCTGATGATGTAAGATGTAAG 2640
Db CGTAACTAGTCTGAGAGTGCCTCAATTTTCTGATGATGTAAGATGTAAG 4641
Qy AAAACAATGTTTCACTGAGAGTGCCTCAATTTTCTGATGATGTAAGATGTAAG 2700
Db AAAACAATGTTTCACTGAGAGTGCCTCAATTTTCTGATGATGTAAGATGTAAG 4701
Qy ATGCTCAATTTTCACTGATGATGTAAGATGTAAGATGTAAGATGTAAG 2753
Db ATGCTCAATTTTCACTGATGATGTAAGATGTAAGATGTAAGATGTAAG 2753


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Db      1682 GAATTTGTCAAAAATATAGACCAAGTATCAAGTGAAGTGTAGAGGGCTGGCCGTGATTCCT 1741
Qy      1741 TATAGTGTGACCTACCCAGAGAGTTATAGAGGAAGCCCACTAAGAACTTTCACATGCT 1800
Db      1742 TATAGTGTGACCTACCCAGAGAGTTATAGAGGAAGCCCACTAAGAACTTTCACATGCT 1801
Qy      1801 GAATTAATCTGCAACATTAATCTGCTGATGCTCACCACCGTGTCCCAATGCTGATGTTG 1860
Db      1802 GAATTAATCTGCAACATTAATCTGCTGATGCTCACCACCGTGTCCCAATGCTGATGTTG 1861
Qy      1861 GCTGTGACTGTGACCTCCCTCTGTCATCTA CTTGGATCTGCTGCTGATCTCAGATGTTG 1920
Db      1862 GCTGTGACTGTGACCTCCCTCTGTCATCTA CTTGGATCTGCTGCTGATCTCAGATGTTG 1921
Qy      1921 TGCCAGTGAACCCAGACTGGGGGCGAGGGCCAGAAATACCTCTTAAGAAATCTCCAAAGA 1980
Db      1922 TGCCAGTGAACCCAGACTGGGGGCGAGGGCCAGAAATACCTCTTAAGAAATCTCCAAAGA 1981
Qy      1981 AACCTCCAGTTTCATGCTTTTATTTATTAATAGTGAACATGATTTCTGCTGGGTGAAGAAT 2040
Db      1982 AACCTCCAGTTTCATGCTTTTATTTATTAATAGTGAACATGATTTCTGCTGGGTGAAGAAT 2041
Qy      2041 GAATTTGTGACCTTACCTAGAAAAAGAGATATACAGATTTGTCTTCATGAGAGAACTTT 2100
Db      2042 GAATTTGTGACCTTACCTAGAAAAAGAGATATACAGATTTGTCTTCATGAGAGAACTTT 2101
Qy      2101 GTCCCTGGAGAAAGCATTTGTGAAATATCATCATCAATGATGAGAGAGTTCAAGTCC 2160
Db      2102 GTCCCTGGAGAAAGCATTTGTGAAATATCATCATCAATGATGAGAGAGTTCAAGTCC 2161
Qy      2161 ATCTTTGTTTGTCTCCCACTTTTGTCCAGAGTGTGGTGGCCATTAAGCACTATTTT 2220
Db      2162 ATCTTTGTTTGTCTCCCACTTTTGTCCAGAGTGTGGTGGCCATTAAGCACTATTTT 2221
Qy      2221 GCCCATCACAATCTCTTTCATGAGAGATTAATTAATCTTATCTTACCTGTAAGCC 2280
Db      2222 GCCCATCACAATCTCTTTCATGAGAGATTAATTAATCTTATCTTACCTGTAAGCC 2281
Qy      2281 ATTCACAGAAACAGACTTCCCAACAAGTACCAACAAGCTGAAGGCTCTCAACGACGCG 2340
Db      2282 ATTCACAGAAACAGACTTCCCAACAAGTACCAACAAGCTGAAGGCTCTCAACGACGCG 2341
Qy      2341 ACTTATTTGCAATGCCCCAAGAGAAAGCAAGCGGCTCTTTGGGCTTAACATTAGA 2400
Db      2342 ACTTATTTGCAATGCCCCAAGAGAAAGCAAGCGGCTCTTTGGGCTTAACATTAGA 2401
Qy      2401 GCCGCTTTTAAATATGAAATTAACACTAGTCACTGAAAAAATGATGTAATCTTAAAAA 2460
Db      2402 GCCGCTTTTAAATATGAAATTAACACTAGTCACTGAAAAAATGATGTAATCTTAAAAA 2461
Qy      2461 AATTTAGGAATTAACCTTAAGAAACCATTAATTA CTTGATGATGATGTAATGATGACGT 2520
Db      2462 AATTTAGGAATTAACCTTAAGAAACCATTAATTA CTTGATGATGATGTAATGATGACGT 2521
Qy      2521 CGTAAGTAACTGTCTGGAGGTGCTCCATTAATCTTCATGAGCTTTCAGAAAGCTTAAACA 2580
Db      2522 CGTAAGTAACTGTCTGGAGGTGCTCCATTAATCTTCATGAGCTTTCAGAAAGCTTAAACA 2581
Qy      2581 AAACAATGTTTCATCTGGGGAACCTAGCTAGAGCGGTGAGGTTAGCTGSCAATTGAGAGC 2640
Db      2582 AAACAATGTTTCATCTGGGGAACCTAGCTAGAGCGGTGAGGTTAGCTGSCAATTGAGAGC 2641
Qy      2641 AGCCAGTCTCTCTTGCTGTTTAATCATTAATGTTTCAATTAATGAAACAGTCTCTTTGAGTAA 2700
Db      2642 AGCCAGTCTCTCTTGCTGTTTAATCATTAATGTTTCAATTAATGAAACAGTCTCTTTGAGTAA 2701
Qy      2701 ATGCTCAAGTTTTCAGCTCCTCTCCACACTGCTTCCCAAAATGAGATTCGTTG 2753
Db      2702 ATGCTCAAGTTTTCAGCTCCTCTCCACACTGCTTCCCAAAATGAGATTCGTTG 2754

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US-09-949-002-65
; Sequence 65, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 2366
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-65

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Query Match      52.5%; Score 1444.2; DB 3; Length 2366;
Best Local Similarity 76.4%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 548; Indels 6; Gaps 1;

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Qy      88 ATTTGTTAAAGCTTCATTTTGTGCTTATGATCATATAGTTGGAGACCAAGATCCAG 147
Db      1 ATGACTAGCATTTTCATTTTCCATTTATCTTCAATGTTATATCTTCAGATCAGAAATACA 60
Qy      148 TTCTCCGACGGAATATGATTTGCACTAGACAGTCAAAAAGAGCTTATTCATGTTCCA 207
Db      61 TTAATGGAAGAAAGGAATTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Qy      208 AAAGACCTTACCGCTGAAAACCAAGCTTTAGATATGCTCAGAACTACATGCTGAGCTT 267
Db      121 AAAGACCTTACCGCTGAAAACCAAGCTTTAGATATGCTCAGAAATATATATCTGAGCTT 180
Qy      268 CAGGCTCTGCAATGAGCTTTCTATCAGAGTTGACAGTTTGAAGCTTCCCATTAACA 327
Db      181 TGGAATCTGCAATGAGCTTTCTATCAGAGTTGACAGTTTGAAGCTTCCCATTAACA 240
Qy      328 ATCCAGTACTGATTAATTAAGTGTTCAGAGTTTCAACCAAGATTTGAATTTGATTTGA 387
Db      241 ATCCAGTACTGATTAATTAAGTGTTCAGAGTTTCAACCAAGATTTGAATTTGATTTG 300
Qy      388 TCTCATTAATCACTTGCAGAAAGATATCTGCATCTTATTTGATGATTTGATGATTTGAT 447
Db      301 TCCCAACAAGTGTGATGATTTCTTGCCACCTTACTGATGATGATGATGATGATGATGAT 360
Qy      448 CTCTCATTAATGATTTTCAAGGCTCTGCCATCTGTAAGAAATTTGGCACTTATACAA 507
Db      361 CTCTCATTAATGATTTTCAAGGCTCTGCCATCTGTAAGAAATTTGGCACTTATACAA 420
Qy      508 CTGAATTTCTTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567
Db      421 CTGAATTTCTTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Qy      568 CACTTGCATCTAAGTTATATCTTCTGATTTTGAAGAAATTTATTAATTAAGAAATGAG 627
Db      481 CACTTGCATCTAAGTTATATCTTCTGATTTTGAAGAAATTTATTAATTAAGAAATGAG 540
Qy      628 ACAGAAAGCTTACAAATTTCTGAATGCAAAAACCTTCACTGTTGTTTTCACCCAACTAGT 687
Db      541 CCGAGGACCTTCAAGACTTTTAAACCTGAGAGTGTGACATTTGTTTCCCAAAACAA 600
Qy      688 TTAATCGCTATCAAGTGAACATATCACTTAATATTAAGGATGTTCAACTGACTAAT 747
Db      601 GAATTCATTTTATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Qy      748 ATTAAT-----TGAATGATGACAACTGTCAAGTTTCAATTAATTTTATCAGAACTC 801
Db      661 ATCAATGTGTGCTAGAAAGATTAACAAATGTTCTTACTTCTTAAGTATCTGCGCAAACTT 720

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QY	802	ACGAGAGTTCAACCTTACTGTAATTTTCCCTCCACCAACATAGAAACGACTTGGAAATGC	861
Db	721	CAACCAAAATCCAAAGTATACAAAGCTTAACTTTAAACAACATTTGAAACAACCTTGAATTC	780
QY	862	CTGGTCAGAGTCTTTCATTTCTTTGGGCCAAACCTGGGAATATCTCAATATTACAAAT	921
Db	781	TTCAATTAGAGATCTCCAGCTGTTTGGCATACACTGATATGTATTTCTCAATTTCAAC	840
QY	922	TTAACATTAATTGAAAGCAATTCGTGAGAAAGATTTTACTTAATCTCAAAAAGCAATTGAA	981
Db	841	GTGAAGCTACAGGGCTCAGCTGGACTTCAGAGATTTTGTATTTCTGGCACTTCCTTGAAG	900
QY	982	GCATTGCAAAATAGAACATATACGAAACCAAGTTTTCGTATTCAACACAGCTTTGAC	1041
Db	901	GCCCTGTCTAATACCAAAAGTGTGCGCATGTGTGGTTTTCCGCAAAATTATATCTAT	960
QY	1042	ACCGGTTTTCTGAGATGAACATTTATGATGTTAACATTTGASATACACTTTATACAC	1101
Db	961	GAAATCTTTTGGAAATATGACATTCAAAAATTTCAAGTGTCTGGTACACGATGGTCCAC	1020
QY	1102	ATGCTGTGTCTCATGACCAAGCAACATTCAGTTTGTAACTTTACCCAGACGTTTTC	1161
Db	1021	ATGCTTTGCCCATCCAAATATAGCCGCTTCGATTTTGATTTTCCAAATATCTGTTA	1080
QY	1162	ACAGATAGTATTTTGGAAAAATGTTCACAGTTAGTTAATTTGGAGACCTTATCTTACA	1221
Db	1081	ACAGACACGGTTTTTGGAAAAATTTGTGGGACCTTATCTGAGTTGGAGACATTAATTTTCA	1140
QY	1222	AAAAATGGAATTAAGACCTTTTCAAAGTAGGTCTCATGAGGAAGGATATGCTCTTGG	1281
Db	1141	ATGAATCAATTTAAAGAACTTTCAAAAATAGCTGAATATGACTACACAGATGAAGTCTGTG	1200
QY	1282	GAAATACTGATGTGTAGCTGGAATTTCTTGGAAATCTGTAGACATTAAGAAACTGTCACT	1341
Db	1201	CAACAAATTTGGATATTAGCAGAAATTTCTGTAAAGCTATGATGAAGAAAGAGAGCTGTCT	1260
QY	1342	TGGGTTGAGATATGTGGTTTAAATTTGTCTCAATATGCTTACCTGACTCTGTTTTC	1401
Db	1261	TGGACTTAAAGTTTATTAAGTTTAAATATGTCTTCAAAATATACCTTACGACACTAATTTTTC	1320
QY	1402	AGATGTTTACCTCCAGAGATCAAGGATCTGTATCTCTCACACAAATTAATAAGAGGGTT	1461
Db	1321	AGATGTTTACCTCCAGAGATCAAGGATCTGTATCTCTCACAGCAATTAATAAGAGCAATT	1380
QY	1462	CCTAACAAGTCTTAAACTGGAGACTTTGCAAGAACATCATGTGCTTTCATTTCTTTA	1521
Db	1381	CCTAACAAGTCTTAAACTGGAGACTTTGCAAGAACCTCATGTGCTTTCATTTCTTTA	1440
QY	1522	ACTGACCTTCTCGATGTGGACGCTTTAGACGCTTTCGTATATGATCATTTGATCAAT	1581
Db	1441	ACTGACCTTCTCGATGTGGACGCTTTAGACGCTTTCGTATATGATCATTTGATCACAAT	1500
QY	1582	TCAGTTTCCCAACCANTGGCTGATTTCTTCCAGAGCTCCGAGGAATAGGTCAAATATAA	1641
Db	1501	TCAGTTTCCCAACCANTAGCTGATTTCTTCCAGAGCTCCGAGGAATAGGTCAAATATAA	1560
QY	1642	GCAGGGGCAATTCATTTCCAAATGTATCTGTGAGCTTAAGAAATTTGTCAAAAAATATAGAC	1701
Db	1561	GCAGGGGCAATTCATTTCCAAATGTATCTGTGAGCTTAAGAAATTTGTCAAAAAATATAGAC	1620
QY	1702	CAAGTATCAAGTAAGTGTAGAGGGCTGAGCTGATCTTATTAAGTGTACTACCCAGAA	1761
Db	1621	CAAGTATCAAGTAAGTGTAGAGGGCTGAGCTGATCTTATTAAGTGTACTACCCGAAA	1680
QY	1762	AGTTATTAAGGAAGCCCAATAAGGACTTTTCACATGTCTGAATTAATCTTGGCAACTAACT	1821
Db	1681	AGTTATTAAGGAAGCCCTACTAAAGGACTTTTCACATGTCTGAATTAATCTTGGCAACTAACT	1740
QY	1822	CTGCTGATCTGATCAGCATCGGTGTCACCAATGCTGTGTGGCTGTGACCTGTACCTCCTC	1881
Db	1741	CTGCTGATCTGATCAGCATCGGTGTCACCAATGCTGTGTGGCTGTGACCTGTACCTCCTC	1800
QY	1882	TGCATCTTATCTTGAGATCTGCTGTATCTCAAGATGATGTGTGCCAGTGGACCCAGACTTCGG	1941

Db	1801	TGCATCTACTTGATCTGCCCTCGTATCTCAGATGTGGTCCAGTGGACCCAAACCCGG	1860
Qy	1942	CGCAGGGCCAGGAACTATCCCTTAGAAGAACTCCAAAGAACTTCCAGTTTCATGCTTTT	2001
Db	1861	CGCAGGGCCAGGAACTATCCCTTAGAAGAACTCCAAAGAAATCTCCAGTTTTCATGCAATTT	1920
Qy	2002	ATTTCATCTAGTGAACATGATTTCTGCCGTGGGTAAGAAAGTGAATTGTAACTTACTCTAGA	2061
Db	1921	ATTTCATCTAGTGGCAGCATTTCTTCTGGGTGAAGATGAATTAATTTGCCAAACTTAGAG	1980
Qy	2062	AAAGAGATATATACGATTTGTCTTCATGAGAGAACTTTGTCCCTGGCAAGACATTTGTG	2121
Db	1981	AAAGAGGTATGCAGATTTGGCTTCATGAGAGAACTTTGTCTCGCGAAGACATTTGTG	2040
Qy	2122	GAAATATATCACTGATTTGAGAAAGATTACAAAGTCCATCTTGTTTGTCTGCCAAC	2181
Db	2041	GAAATATATCACTGATTTGAGAAAGATTACAAAGTCCATCTTGTTTGTCTGCCAAC	2100
Qy	2182	TTTGTCCAGAGTGGTGGCTTATAGCACTCATTTTGGCCATCAACAATCTCTTTCAT	2241
Db	2101	TTTGTCCAGAGTGGTGGCTTATAGCACTCATTTTGGCCATCAACAATCTCTTTCAT	2160
Qy	2242	GAAAGATCTAATTAATTATCTTCATCTTACTGAAACCATTTCCACAGAACGATTTCC	2301
Db	2161	GAAAGATCTAATTAAGTTATCTTCATCTTCTGGAACCATTTCCGAGTATCTCATTTCT	2220
Qy	2302	AACAAGTCCCAAGCTGAAAGGCTCTATAGCGAGGGGACTTATTTTGCAGTGGCCCAAG	2361
Db	2221	AGCAGTTATTCACAGCTCAAAAGTCTCATGGCCAGAGAGACTTATTTTGGATTTGGCCCAAG	2280
Qy	2362	GAGAAAGCAAAAGCTGGGCTTTTGGGCTTAACATTAGAGCCGGCTTTTAATATGAAATTA	2421
Db	2281	GAAAAAGCAAAAGCTGGGCTTTTGGGCTTAACATTAGAGGAGCCATTAATATTAAGCTG	2340
Qy	2422	ACA 2424	
Db	2341	ACA 2343	

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RESULT 6
US-09-949-002-236
; Sequence 236, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 2367
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2367)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-236

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	Query Match	Score	DB 3	Length
Query Match Similarity	51.8%	1426.4		2367
Best Local Similarity	76.1%	Fred. No. 0		
Matches 1785; Conservative	0;	Matches 552;	Indels 8;	Gaps 2;

	Qy	Db
88	ATTGTTAAAGCTTCATTGTTGTTGCTTAGATCATTAATGTTGGACCAAGAAATCCAG	147
1	ATGACTACACATCTTCATTGTCATTCATGTTAAATCACTTCAGATCAGAAATACAA	60

QY 148 TTCTCGACGGAATGATTTTGAGTAGCAAGTCAAAAAGAGCTTATTCATGTTCCA 207
 Db 61 TTATCTGAAGAAAGTAAATTTTGTAGTAGGTCAAAAACGGTCTCATCCAGTTCCT 120
 QY 208 AAAAGACTTACCGGTGAAAAACAAGCTTAGATATGTCAGAACTACATCGCTGAGCTT 267
 Db 121 AAAAGACTTACCGGTGAAAAACAAGCTTAGATATGTCAGAACTACATCGCTGAGCTT 180
 QY 268 CAGGCTCTGACATGAGCTTTCTATCAGAGTTGACAGTTTGGACTTTCCCATTAACA 327
 Db 181 TGGACTCTGACATGAGCTTTCTATCAGAGTTGACAGTTTGGACTTTCCCATTAACA 240
 QY 328 ATCCAGCTACTGATTTAGTGTGTTTCAAGTTCAACGAGATTTTAATATTTGATTTA 387
 Db 241 ATCCAGCTACTGATTTAGTGTGTTTCAAGTTCAACGAGATTTTAATATTTGATTTA 300
 QY 388 TCTCATTAATCAGTTGCAAAAAGATATCTGCAATCC--TATTTGAGTTTCAAGCATTTAG 445
 Db 301 TCCCACAAAAAGTTGGTGAAGATTTCTTGCAACCCCTACTGTGAACCCCTCAGCACTTGG 360
 QY 446 ATCTCTCATTAATGATTTCAAGGCTTGCCTGCTGTAAGGAATTTGGCAACTTATCAC 505
 Db 361 ACCGTCTATTAATGATTTGAATGCTGCTGCTATATGCAAGAGTTTGGCAATATGCTTC 420
 QY 506 AACTGAAATTTCTGGGATGAGTGTATGAGCTGCAAAAATTAGATTTGCTGGCAATTG 565
 Db 421 AACTGAAATTTCTGGGATGAGTGTATGAGCTGCAAAAATTAGATTTGCTGGCAATTG 480
 QY 566 CTCACTTCATCTAAATGATTAATCTTCTGATTTAAGAAATTAATTAATTAAGAAATG 625
 Db 481 CTCACTTCATCTAAATGATTAATCTTCTGATTTAAGAAATTAATTAATTAAGAAATG 540
 QY 626 AGACAGAAAGTCTCAAAATTTGATGCAAAAACCTTCACTTGTGTTTTCACCCAACTA 685
 Db 541 ACCCTGAGGGCTTCAAGACTTTTAACTAGAGAGTCTGCAATGTTGTTCCCAACAACA 600
 QY 686 GTTATTTGGCTATCCAGAGAACATATCTGTTAATCTTAGAGTCTTACAATGACTA 745
 Db 601 AAGAAATTCATTTTATTTTGTGATGTCTGATGCAAGCTGATGCAAACTGGAATCTTA 660
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 Db 1381 TTCTTAACAAAGTGTGTAAGCTGGAAGCTTTGCAAGAACTCAATGTGCTTCAATCTT 1440
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 Db 1441 TAACTGACTTCTGATGTGCGAGCTTTAGACAGCTTTCTGTATTTGATCATTTGATACA 1500
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 Db 1561 AAGCAGGGGACATCCATTCATGTAATCTGTAGCTAAGAGAAATTTGTCAAAAATATAG 1620
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 Db 1621 ACCAAGTATCAAGTGAAGTGTAGAGGCTGCGCTGATTTCTTAATAGTGTACTACCCAG 1680
 QY 1760 AAGATTAAGAGAAAGCCCAATAAGAACTTCAATGTCTGAATTAATCTGCAACATA 1819
 Db 1681 AAGATTAAGAGAAAGCCCAATAAGAACTTCAATGTCTGAATTAATCTGCAACATA 1740
 QY 1820 CTCTGCTGATCTGCAACATCGGTGACCAACATCTGATGTTGGCTGATCTGACTGCTCCC 1879
 Db 1741 CTCTGCTGATCTGCAACATCGGTGACCAACATCTGATGTTGGCTGATCTGACTGCTCCC 1800
 QY 1880 TCTGATCTACTTGGATCTGCCCTGTGTATCTCAGATGTGTGCCAGTGTGACCCAGATCTC 1939
 Db 1801 TCTGATCTACTTGGATCTGCCCTGTGTATCTCAGATGTGTGCCAGTGTGACCCAGATCTC 1860
 QY 1940 GGGCGAGGGCCAGGAACATACCTTGAAGAACTCCAAAGAAACCTCCAGTTTCATGCTT 1999
 Db 1861 GGGCGAGGGCCAGGAACATACCTTGAAGAACTCCAAAGAAACCTCCAGTTTCATGCTT 1920
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Db 2221 CTAGCAGTTATCACAAGCTCAAAAGTCTCATGCGCAGAGGACTTAATTTGGATGCCCCA 2280
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Oy 2420 TAACA 2424
Db 2341 TGACA 2345

RESULT 7
US-09-949-002-637
; Sequence 637, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 637
; LENGTH: 6392
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1) - (6392)
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-002-637

Query Match 50.6%; Score 1392; DB 3; Length 6392;
Best Local Similarity 75.3%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 552; Indels 33; Gaps 3;

Oy 88 ATTGTTAAAGCTTCCATTTTGTGCTTATGATCATATATGTTGAACCAATCCAG 147
Db 2001 ATGACTAGCATCTTCATTTGCCATTATCTTCATGTTAATCTTCAGATCAGAAATACAA 2060
Oy 148 TTCTCCGACGAAAGATTTGCAGTAGCAAGTCAAAAGAGCTTTTATGATGTTCA 207
Db 2061 TTATCTGAAGAAAGTGAATTTTATGTTAGTAGAGTCAAAAACGCTCTCATCCAGTTCT 2120
Oy 208 AAAGACTACGCTGAAAAACAAGCTTAGATATGTCAGAACTACATCGCTGAGCTT 267
Db 2121 AAAGACTATCCCAAGAAACAACATCTTAATATATGCCAAATATATATCTGAGCTT 2180
Oy 268 CAGTCTCTGACATGAGCTTTCTATCAGAGTTGACAGTTTGAAGCTTTCCATAACAGA 327
Db 2181 TGGAATCTGACATCTTATCAGTCAAAAGTGAAGATTTGATATTTCTCATATATAGA 2240
Oy 328 ATCCGACTACTGATTTAAGTTTTCAGAGTTCAACCGAGATTTAGAAATTTGAGTTTA 387
Db 2241 ATCCGATATCTTGAATATCAGTGTTCAAATTCACAGAGAAATGGAAATCTTGAATTTG 2300
Oy 388 TCTCATATTC-----AGTTGAAAGATATCCGCGCATCC 422
Db 2301 TCCCAAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2360
Oy 423 --TATGTAGATTTCAGGCAATTAGATCTCTCATTCATGATTTCAAGGCCCTGCCATC 480
Db 2361 CTAGTGAACCCCTCAAGCACTTGGACGTGTCATTTAATGCAATTTGATGCCCTGCTANA 2420
Oy 481 TGTAGGAATTTGGCACTTATCACAACCTGAATTTCTTGGAGTTGAGTCTATGAAGCTG 540
Db 2421 TGCAAGAGTTGGCAATATGTCACAATMAAATTTCTGGGGTTGAGCACACACACTTA 2480
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Oy 601 AGAAATATATATATAAAGAAATAGACAGAAAGTCTCAAAATCTGATAGCAAAAAAC 660
Db 2541 GGAGAGACTTATGGGAAAAAGAAAGCCGTGAGGGCTTCAGACTTTAACACTGAGAGT 2600
Oy 661 CTTCACCTTGTCTTTCACCCAACTAGTTATTCGCTATCCAGTGAACATATCACTTAAT 720
Db 2601 CTGACATTTGCTTCCCAACAAAGAAATTTCCATTTATTTTGGAGTGTGACATCAAG 2660
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Db 2661 ACTGAGCAAAATCTGAACTATCTAATATCAATGTGTGATAGATGACAAATGTTCT 2720
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Db 2781 AACCACTAGAAACACTTGGAAATCTTTCATTAAGATCTCCAGCTGTTGGCATACA 2840
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Oy 1315 TCTGTAGACATTAAGAAACCTGACCTTGGGTGAGATATGAGTATTAATTTGCT 1374
Db 3261 TATGATGAAAGAAAGAGAGCTGTTCTTGGACTAATAATTTAATTAATATGCT 3320
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Db 3441 GAACCTAATGTTGCTTTCAATTTCTTAACTGACCTTCTGATGTGCGAGCTTTAGCAGC 3500
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Db 3501 CTTCCTGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3560
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QY 1615 AGCTGCAGAGATGAGTCAATTAAGAGAGGAGCAATCCATCTCAATGTACTGTAG 1674
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QY 1675 CTAAAGAAATTTGTCAAAATATAGCAAGTTCAGTGAAGTGTGAAGGGCTGGCT 1734
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DB 3621 CTAGGAGAAATTTGTCAAAATATAGCAAGTTCAGTGAAGTGTGAAGGGCTGGCT 3680
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QY 1735 GATTCCTTAAGTGTACTACCCAGAAAGTATAGAGAAAGCCCAATAAGACTTTCAC 1794
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DB 3681 GATTCCTTAAGTGTACTACCCAGAAAGTATAGAGAAAGCCCAATAAGACTTTCAC 3740
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QY 1795 ATGTCTGAATTAATCTCGCAACATTAATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1854
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QY 1855 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1914
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DB 3801 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3860
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QY 1915 ATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1974
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DB 3861 ATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3920
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QY 1975 CAAAGAAACCTCCAGTTCATCTTATTTATATATGAATGAATTTCTGCTGGGTG 2034
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QY 2035 AAAAGTAATGTGTACTTACCTAGAAAGAAATATACAGATTTGTCTTGTGTGTGTGT 2094
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QY 2095 AACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2154
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QY 2155 AAGTCATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2214
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QY 2215 TATTTTGGCCATCAATCTCTTTCATGAAGATCTTAATTAATCTTCAATCTTACTG 2274
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DB 4161 TATTTTGGCCATCAATCTCTTTCATGAAGATCTTAATTAATCTTCAATCTTACTG 4220
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QY 2275 GAACCATTTCCAGAGAGCATTTCCCAATTCAGATGAGTGTGTGTGTGTGTGTGTGT 2334
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DB 4221 GAACCATTTCCAGAGAGCATTTCCCAATTCAGATGAGTGTGTGTGTGTGTGTGTGT 4280
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QY 2335 CAGCGGACTTATTTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2394
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DB 4281 CAGCGGACTTATTTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4340
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QY 2395 ATTAGAGCGCTTTTAAATGAATTAACA 2424
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DB 4341 ATTAGAGCGCTTTTAAATGAATTAACA 4370
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RESULT 8
US-09-949-002-808
; Sequence 808, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CLO000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 808
; LENGTH: 6392
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (6392)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-808

Query Match      50.6%; Score 1392; DB 3; Length 6392;
Best Local Similarity 75.3%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 552; Indels 33; Gaps 3;

QY 88 ATTTGTAAGCTTCATTTTGTGTCCTTATGATCATATATAGTGAACGAATCCG 147
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QY 148 TTCTCCGACGGAATGAAATTTGCACTAGCAAGTCMAAAAGAGCTTATTCATGTCCA 207
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DB 2061 TTATCTGAAGAAAGTGAATTTTATGTGATAGTCAAAAAGGCTCATCCAGTTCCT 2120
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QY 208 AAAAGCTACCGCTGAAAACAAAGTCTTGAATGTCTCAGACTACATCGCTGAGCTT 267
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DB 2121 AAAAGCTACCGCTGAAAACAAAGTCTTGAATGTCTCAGACTACATCGCTGAGCTT 2180
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QY 268 CAGGCTCTGACATGAGCTTTATCAGAGTTGACAGTTTGAAGCTTCCATTAACGA 327
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QY 328 ATCCAGCTATCTGATTAATGATTTTCAAGTTCAACAGATTTGAATTTGATTTGA 387
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QY 481 TGAAGAAATTTGGAACTTATCAACATGAATTTCTTGAGATGAGTGTGTGAAGCTG 540
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DB 2541 AGAAATTAATTAATTAAGAAATTAAGACAGAAAGTCAAAATTTCTGAATGCAAAAAC 2600
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DB 2601 CTGACCTTGTGTTTTCACCCAACTAGTTTATTCGCTATCAAGTGAACATCATGTTAAT 2660
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QY 721 ACTTTAGGAGTGTCAACCTGATATATTAAT-----TGAATGATGACACTGTCA 774
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DB 2721 TACTTCTTAAGTATTTCTGCGAACTTCAACAAATTCAGAGTTTCAAAATTTTACCTTA 2780
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QY 835 AACCATGAAGAAACGACTTGAATGCTGTGACAGAGCTTTCATTTCTTTGGCCCAA 894
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DB 2781 AACCATGAAGAAACGACTTGAATGCTGTGACAGAGCTTTCATTTCTTTGGCCCAA 2840
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DB 2841 ACTGTATGTATTTTCTCAATTTTCAAACTGAAGCTAAGGCTCAAGCTTCAAGAT 2900
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Qy	955	TTTACTTATCTTAAAGACGACATGGAAGCATTTGACAAATAGAACATATACGACGACAGTT	101.4
Dp	2901	TTTGATTATTTCTGGGACCTTCTTGAAAGCCTTGTTCTATACCAAGATTGTCAAGCATGTG	296.6
Qy	1015	TTTCTGTTTTACAGACAGCTTTGTACACGCTGTTTTCTGAGTGAACATATAGATTTA	107.4
Dp	2961	TTTCGTTTTCCGCAAGATTATATCTATGAAATCTTTTGGAAATATGAACATCAAAATTTTC	302.0
Qy	1075	ACCAATTCAGATPACCTTTTATATACATNGCTGTCTCATGCAACCAAGACATTCAG	113.3
Dp	3021	ACAGGTTGTGGACACGCGATGGTCCACAGCTTGCCCATCCAAATTAGCCCGTTCTG	308.6
Qy	1135	TTTTTGAACCTTACCCAGACGTTTTTCACAGATAGATTTTTTGGAAAAATGTTCCAGTTA	119.2
Dp	3081	CATTGGATTTTTTCCAAATATCTCTTAAACAGACAGTTTTTGAATAATGTGGGCACTT	314.0
Qy	1195	GTTAAATTTGGAGACACTTATCTTACAAAAAATGATTTAAAGACCTTTTCAAGTAGCT	125.5
Dp	3141	ACTGAGTTGGAGACACTTATTTTTACMAATGATCAATTTAAAGAACTTTCAAAAATACCT	320.0
Qy	1255	CTCATGACGAAGGATATGCTCTTTTGGAAATACAGATGATAGTGGAAATCTTTGGAA	131.4
Dp	3201	GAAATGACTACACAGATGAAGTCTCTGCAACATTTGATATTTAGCCAGAAATTTCTTAAGC	326.6
Qy	1315	TTCTGTAGACATPAAAGAAAACTGACCTTGCGTTGAGATATAGTGTAAATTTGTCT	137.4
Dp	3261	TATGATGAAAAAGAAAGAGACCTGTTCTTGGACATAAAAGTTTATTAAGTTTAAATATGCT	332.0
Qy	1375	TCAAAATATGCTTACGACTCTGTTTTCAGATGTTTACTCTCCAGAGATCAAGATATTGAT	143.3
Dp	3321	TCAATATATCTACTGACACTATTTTTACAGATGTTTACTCTCCAGGATCAAGGATCTTAT	338.0
Qy	1435	CTTCACAGCAATPAAATATAAGAGCCTTCTTAAACAAGTGTAAACTGGAAGCTTTGCA	149.2
Dp	3381	CTTCACACACATPAAATATAAGGACATTCCTTAAACAAGTGTAAACTGGAAGCTTTGCA	344.4
Qy	1495	GAACTCAAATGTTGCTTTCAATTTCTTTAACTGACTTCTCGATGTGGACGTTTAGCAGC	155.5
Dp	3441	GAACTCAAATGTTGCTTTCAATTTCTTTAACTGACTTCTCGATGTGGACGCTTAGCAGC	350.0
Qy	1555	CTTTCTGATATGATCATATGATACACAATTCAGTTTTCCACCACATGGGCTGATTTCTTCCAG	161.4
Dp	3501	CTTTCTGATATGATCATATGATACACATTCAGTTTTCCACCACATGGGCTGATTTCTTCCAG	356.6
Qy	1615	AGCTGCCAGAAAGATGAGGTCAATPAAACAGAGGGAACAATCCATTTCCAAATGTAACCTGTAG	167.4
Dp	3561	AGCTGCCAGAAAGATGAGGTCAATPAAACAGAGGGAACAATCCATTTCCAAATGTAACCTGTAG	362.2
Qy	1675	CTAAGAGAAATTTGTCTAAAAATATAGACCAAGTATTAAGTGAAGTTTAGAGGGCTGCGCT	173.3
Dp	3621	CTAAGAGAAATTTGTCTAAAAATATAGACCAAGTATTAAGTGAAGTTTAGAGGGCTGCGCT	368.0
Qy	1735	GATTTCTTAAAGTGTGACTACCCAGAAAGTTATAGAGAGGCCACTAAAGACCTTTGAC	179.2
Dp	3681	GATTTCTTAAAGTGTGACTACCCAGAAAGTTATAGAGAGGCCACTTAAAGACCTTTGAC	374.4
Qy	1795	ATGTCGTGAATTATCTGCAACAATACTCTGCTGATGTCACCATGTGTCACCATGCTG	185.4
Dp	3741	ATGTCGTGAATTATCTGCAACAATACTCTGCTGATGTCACCATGTGTCACCATGCTGCT	380.0
Qy	1855	GTTGTTGGCTGTGACGTGACCTCCCTGCAATCTAAGTGAATCTGCGCCCTGGATATCTCAG	191.4
Dp	3801	GTTGTTGGCTGTGACGTGACCTCCCTGCAACTAAGTGAATCTGCGCCCTGGATATCTCAG	386.6
Qy	1915	ATGCTGTGCCAGTGGACCCAGACTTCGCGGCAAGGGCCAGAGAACTATACCTTGAAGAACTC	197.4
Dp	3861	ATGCTGTGCCAGTGGACCCAGACCCGGGCAAGGGCCAGAGAACTATACCTTGAAGAACTC	392.2
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Oy		2395	ATTAGAGCCGCTTTAATATGAATTAACA	2424
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 RESULT 9 US-09-991-181-56 Sequence 56, Application US/09991181 Patent No. 6913919 GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David APPLICANT: Desnovers, Luc APPLICANT: Eaton, Dan L. APPLICANT: Ferrara, Napoleone APPLICANT: Fong, Sherman APPLICANT: Gerber, Hanspeter APPLICANT: Gottlieb, Mary E. APPLICANT: Goddard, Audrey APPLICANT: Grimaldi, Paul J. APPLICANT: Gurney, Austin L. APPLICANT: Kjaevan, Ivar J. APPLICANT: Napier, Mary A. APPLICANT: Pan, James APPLICANT: Paoni, Nicholas F. APPLICANT: Roy, Margaret Ann APPLICANT: Stewart, Timothy A. APPLICANT: Tumas, Daniel APPLICANT: Watanabe, Colin K. APPLICANT: Williams, P. Mickey APPLICANT: Wood, William I. APPLICANT: Zhang, Zemin TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OR INVENTION: Acids Encoding the Same FILE REFERENCE: P2730FIC53 CURRENT APPLICATION NUMBER: US/09/991,181 CURRENT FILING DATE: 2001-11-16 PRIOR APPLICATION NUMBER: 60/049787 PRIOR FILING DATE: 1997-06-16 PRIOR APPLICATION NUMBER: 60/062250 PRIOR FILING DATE: 1997-10-17 PRIOR APPLICATION NUMBER: 60/065186 PRIOR FILING DATE: 1997-11-12 PRIOR APPLICATION NUMBER: 60/065311 PRIOR FILING DATE: 1997-11-13 PRIOR APPLICATION NUMBER: 60/066770 PRIOR FILING DATE: 1997-11-24				

;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR APPLICATION NUMBER: 60/091978
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;; PRIOR FILING DATE: 1998-07-09

Query Match 28.2%; Score 777.2; DB 3; Length 3462;
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Matches 1456; Conservative 0; Mismatches 948; Indels 30; Gaps 8;

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 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerltzen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 28.2%; Score 777.2; DB 3; Length 3462;
Best Local Similarity 59.8%; Pred. No. 3e-209;
Matches 1456; Conservative 0; Mismatches 948; Indels 30; Gaps 8;

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 / Sequence 56, Application US/09989735
 / Patent No. 6972185
 / GENERAL INFORMATION:
 / APPLICANT: Ashkenazi, Avi J.
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan L.
 / APPLICANT: Ferrara, Napoleone
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gerber, Hanspeter
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC61
CURRENT APPLICATION NUMBER: US/09/989,735
PRIOR FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1998-06-24

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RESULT 14
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; Sequence 56, Application US/09989726
; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C60
CURRENT APPLICATION NUMBER: US/09/989,726
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Query Match 28.2%; Score 777.2; DB 5; Length 3462;
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RESULT 15
US-09-997-514-56

Sequence 56, Application US/09997514
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
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APPLICANT: Tumas, Daniel
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C46
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Query Match      28.2%; Score 777.2; DB 5; Length 3462;
Best Local Similarity 59.8%; Pred. No. 3e-209;
Matches 1456; Conservative 0; Mismatches 948; Indels 30; Gaps 8;

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DB 1088 GACATTAAGAAACCTGCAATTAATCAAAATGCAAAATGCAACAGCATTTTCCGAATTA 1147
QY 1119 ACCAAGCATTCAAGTTTGTGAATTTTACCAGAACTTTTCCAGATGAGATTTTGA 1178
DB 1148 TCTTACGAATTTCCAAATTTTAAATTTTGGCCAAATTAATCTTAACAGACGAGTGTTHA 1207
QY 1179 AAATGTTCACGTTAGTTAAATTTGAGACACTTATCTTACAAAAAATGATTAAGA 1238
DB 1208 AAGACATATCCAACTGCTCACTGMAAACTCTATTTTGAATGCAATTAATCTGGAAC 1267
QY 1239 CTTTTCAAAGTAGGTCTATGACGAGATATGCTTTTGAATAATAGATGTTAG 1298
DB 1268 ACTTCTTTAGTAACTGCTTTGCTTACACACAC--CTTGAACACTTGGATCTAG 1324
QY 1299 CTGAATCTTTTGAATCTGATGACATTAAGAAATCTGACCTTGGGTTGAGAGTATAGT 1358
DB 1325 TCAAAATCTATTTACAC--ATTAATAATGATGAATAATGCTCATGCGCAAGAACTGTGT 1381

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Qy 1359 GGTGTTAAATTTGCTTCAGAAATATGCTTACTGACTCTGTTTTTCAGATGTTTACCTCCAG 1418
Db 1382 CAATATGATCTGTATCAATTAATATGTCGTATTCGTCTTCAGGGCTTCCCAAAAG 1441
Qy 1419 GATCAAGGTACTTGATCTTCACAGCAATTAATTAAGAGCGTTCTTAAACAAGTGTAA 1478
Db 1442 TATTCAAATVACTGTGACCTTAATTAATTAACCAATTCCAATCTGTAATTAAGACATTTCA 1501
Qy 1479 ACTGAGAGCTTGAAGAATCAATGTTGCTTCAATCTTAACTGACCTTCGAGATG 1538
Db 1502 TCTGATGGCTTACAGAACTAAATATGCAATTAATTTCTAATCTGATCTCCCTGATG 1561
Qy 1539 TGGCAGCTTTAGCAGCCTTTCTGTATGTATCAATGATCAAAATTCAGTTCCACCCATC 1598
Db 1562 CAGTATTTCAATGATCTTTGCTGTGAACTGAAATGAATTCATTTCTCAGCCCATC 1621
Qy 1599 GAGTGAATTTCTTCCAGAGCTGCCAGAGATGAGGTCAATTAAGAGAGGAGCAATTCATT 1658
Db 1622 TCTGATTTTGTTCAGAGCTGCCAGAGATTAATCTTAATGCGGGAAGAAATCCATT 1681
Qy 1659 CCAATGTCCTGTGAGCTTAAGAAATTTGTCAAAAATATAGACCAAGTATCAAGTAAAT 1718
Db 1682 CCGGTGTACCTGTGAATTA---AAAATTTCAATTCAGCTTGAACATTTCAAGGTCAAT 1738
Qy 1719 GTTAGAGGAGCTGGCCTGATTTCTTATAGTGTGACTAACCCAGAAAGTTATAGAGAAAGCC 1778
Db 1739 GATGTTGGATGTTGATGATTAATCAACCTGTGAATACCTTTAAACCTTAAGGGAACTAG 1798
Qy 1779 ACTAAAGACCTTTCACATGCTCGAATTTATCTGCAACATTAATCTGCTGATGTCACCAT 1838
Db 1799 GTTAAAGACGTTCAATCTCCAGAAATTAATCTTGCAACACAGCTGTGTGATTTGTCAACAT 1858
Qy 1839 CGGTGCCACATGCTGTGTGTGGCTGTGACTGTGACCTCCCTGTGATCTACTTGATCT 1898
Db 1859 TGTGTTATTTATGCTAGTTCCTGGGTTGGCTGTGGCTTCTGTCTCTCCACTTGAATCT 1918
Qy 1899 GCCCTGTATCTCAGAGATGTTGTCAGTGAACCCAGACTCGGCGAGGGCCAGAAACAT 1958
Db 1919 GCCCTGTATCTCAGAGATGTTGTCAGTGAACCCAGACTCGGCGAGGGCCAGAAAC 1978
Qy 1959 ACCCTTGAAGACCTTCAGAAACCTCCAGTTTCAATGCTTTTATTTTCAATATAGTGAACA 2018
Db 1979 AACCCAGAACCACTCAAGAGAAATGTCGATTCACAGCATTTATTTTCAATACGTGAACA 2038
Qy 2019 TGATTTCTGCTGGGGAAGAAATGTTGTTGCTTACCTAGAAAGAAAGAA-----TAT 2072
Db 2039 TGATTTCTGCTGGGGAAGAAATGTTGTTGCTTACCTAGAAAGAAAGATGTTCTAT 2098
Qy 2073 ACAGATTTGCTTTCATGAGAGAACTTTGTCCTGGCAAGACATTTGGAATAATCAT 2132
Db 2099 CTTGATTTGCCCTTTATGAAGCTTACTTTGACCCTGGCAAAAGCAATTAAGTGAATAATGTT 2158
Qy 2133 CAATCTCATGAGAGAGTTCAAGTCCATCTTTGTTGTTCTCCCACTTTGTCCAGAG 2192
Db 2159 AAGCTTCATGAGAAAGCTATATAGTCCATCTTTGTTGTTCTCCCACTTTGTCCAGAA 2218
Qy 2193 TGAGTGGGCAATTAAGAACTATTTTGGCCATCAATCTTTCAATGAAGATCTAA 2252
Db 2219 TGAGTGGGCAATTAAGAACTATTTTGGCCATCAATCTTTCAATGAAGATCTTA 2278
Qy 2253 TAACTTAAATCTCATCTTACTGAAACCAATTCACAGAACAGCATTTCCCAAGTACCA 2312
Db 2279 TCATATTAATCTTACTTACTGAAACCAATTCATTTGATTTCCACAGATATCA 2338
Qy 2313 CAAGCTGAAGCTCTCATGAGCGAGCGGCACTTATTTGAGTGGCCCAAGAGAGAGAAAGCA 2372
Db 2339 TAAACTGAAGCTCTCTGGAAGAAAGCAATATGGAATGCGCCAAAGATAGCGTAA 2398
Qy 2373 ACGTGGGCTTTTGGGCTTAAATATAGAGCGCTTTTATATGAATTAACACTAGTCAAC 2432
Db 2399 ATGTGGGCTTTTCTGAGCAACCTTGAGCTGTATTAATGTTAATGTTAGCCACAG 2458

Qy 2433 TGAAAAACAATGATGTGAATCTTAAAAAAATTTA 2466
Db 2459 AGAAATGTATGAACCTGCAGACATTCACAGAGTTA 2492
Search completed: June 5, 2006, 02:47:52
Job time : 536 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 2, 2006, 22:53:23 ; Search time 157 Seconds
(without alignments)
4689.888 Million cell updates/sec

Title: US-10-732-796a-12

Perfect score: 4154

Sequence: 1 MTKDKRPIVKSFPVCLMI.....IRAFNMKLTVTENNVDVKS 796

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4149	99.9	796	1	TLR6 HUMAN
2	3374	81.2	796	1	O59H16 sus scrofa
3	3361	80.9	796	2	O76L23 pig
4	3315	79.8	793	2	O704V6 BOVIN
5	3306	79.6	793	2	O706D2 BOVIN
6	3147.5	75.8	806	2	O6P690 RAT
7	3144.5	75.7	795	1	TLR6 MOUSE
8	3144.5	75.7	806	2	O3UV88 mus musculus
9	3143.5	75.7	806	2	O7TPC5 MOUSE
10	2830	68.1	786	1	TLR1 HUMAN
11	2830	68.1	786	2	O32MK3 HUMAN
12	2829	68.1	786	2	O32MK4 HUMAN
13	2828	68.1	786	2	O5FMG5 HUMAN
14	2817	67.8	786	2	O6F164 HUMAN
15	2654.5	63.9	796	2	O4UDR7 pig
16	2654.5	63.9	796	2	O5SH19 pig
17	2525	60.8	795	1	TLR1 MOUSE
18	2468	59.4	727	2	O6A0E8 MOUSE
19	2400	57.8	727	2	O6GCV21 BOVIN
20	2322	55.9	480	2	O2MK13 HUMAN
21	1967	47.4	818	2	O5WA51 CHICK
22	1965	47.3	818	2	O5T1H8 CHICK
23	1905.5	45.9	811	2	O5FMG4 HUMAN
24	1902.5	45.8	811	1	TLR10 HUMAN
25	1899.5	45.7	811	2	O32MI8 HUMAN
26	1896.5	45.7	811	2	O32MI7 HUMAN
27	1850.5	44.5	811	2	O4UDR6 pig
28	1838	44.5	811	2	O5SH15 pig
29	1838	44.2	812	2	O6GCV17 BOVIN
30	1421	34.2	389	2	O8C1X4 CRIGR
31	1246.5	30.0	812	2	O5H727_FUGRU

32	1227	29.5	789	2	O4R2C3 TETNG	O4R2C3 tetradon n
33	1050	25.3	227	2	O56GY4 BOVIN	O56GY4 bos taurus
34	1050	25.3	227	2	O56GZ4 SHEEP	O56GZ4 ovis aries
35	1043.5	25.1	258	2	O3BR20 BOVIN	O3BR20 bos taurus
36	963.5	23.2	784	1	TLR2 MOUSE	O9QU07 mus musculus
37	963.5	23.2	784	2	O3U400 MOUSE	O3U400 mus musculus
38	963.5	23.2	784	2	O811T5 MOUSE	O811T5 mus musculus
39	962.5	23.2	784	2	O8X3D9 MOUSE	O8X3D9 mus musculus
40	951.5	22.9	784	2	O6YGU2 RAT	O6YGU2 rattus norv
41	946	22.8	784	1	TLR2 HUMAN	O60603 homo sapien
42	945.5	22.8	785	2	O76L24 pig	O76L24 sus scrofa
43	943.5	22.7	784	1	TLR2 CRIGR	O9X1F8 cricetus
44	943.5	22.7	785	2	O59H18 pig	O59H18 sus scrofa
45	940.5	22.6	785	2	O6TN21_PIG	O6TN21 sus scrofa

ALIGNMENTS

RESULT 1
TLR6_HUMAN STANDARD, PRT, 796 AA.
AC Q9Y2C9;
DT 31-JAN-2002, integrated into UniprotKB/Swiss-Prot.
DT 01-NOV-1999, sequence version 1.
DT 07-MAR-2006, entry version 42.
DE Toll-like receptor 6 precursor.
GN Name=TLR6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Placenta;
RX MEDLINE=99250250; PubMed=10231569; DOI=10.1016/S0378-1119(199)00098-0;
RA Takeuchi O., Kawai T., Sanjo H., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Takeda K., Akira S.;
RT "TLR6: a novel member of an expanding Toll-like receptor family.";
RL Gene 231:59-65(1999).
RN [2]
RP FUNCTION.
RX MEDLINE=21334385; PubMed=11441107;
RA Bulut Y., Faure B., Thomas L., Equils O., Arditi M.;
RT "Cooperation of Toll-like receptor 2 and 6 for cellular activation by
soluble tuberculosis factor and Borrelia burgdorferi outer surface
protein A lipoprotein: role of Toll-interacting protein and IL-1
receptor signaling molecules in Toll-like receptor 2 signaling.";
RL J. Immunol. 167:987-994(2001).
CC -!- FUNCTION: Participates in the innate immune response to Gram-
positive bacteria and fungi. Acts via MyD88 and TRAF6, leading to
NF-kappa-B activation, cytokine secretion and the inflammatory
response. Recognizes mycoplasma macrophage-activating
lipopeptide-2kD (MALP-2), soluble tuberculosis factor (SFP),
phenol-soluble modulin (PSM) and B.burgdorferi outer surface
protein A lipoprotein (OspA-L) cooperatively with TLR2.
CC -!- SUBUNIT: Binds TLR2 via their respective extracellular domains.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
phagosomes (by similarity).
CC -!- TISSUE SPECIFICITY: Detected in monocytes, CD11c+ immature
dendritic cells, plasmacytoid pre-dendritic cells and dermal
microvessel endothelial cells.
CC -!- SIMILARITY: Belongs to the Toll-like receptor family.
CC -!- SIMILARITY: Contains 13 IRR (leucine-rich) repeats.
CC -!- SIMILARITY: Contains 1 TIR domain.
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DR EMBL, AB020807; BAAV7631.1; -, mRNA.
DR HSPB, Q15399; 1FVY.

DR SMR; Q9Y2C9; 630-786.
 DR Ensembl; ENSG00000174130; Homo sapiens.
 DR HGNC; HGNC:16711; TLR6.
 DR MIM; 605403; gene.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0016020; C:membrane; ISS.
 DR GO; GO:0045335; C:phagocytic vesicle; ISS.
 DR GO; GO:0008034; F:lipoprotein binding; ISS.
 DR GO; GO:004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007250; P:defense response to bacteria; TAS.
 DR GO; GO:0042742; P:defense response to bacteria; TAS.
 DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR GO; GO:0042116; P:macrophage activation; ISS.
 DR GO; GO:0045410; P:positive regulation of interleukin-12 biosyn. . .; ISS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR GO; GO:0042088; P:T-helper 1 type immune response; IC.
 DR InterPro; IPR004075; IL1_rcpt_1.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_C.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00560; LRR_1; 8.
 DR Pfam; PF01463; LRRCT; 1.
 DR PRINTS; PR01582; TIR; 1.
 DR PRINTS; PR01537; INTRIKRI1.F.
 DR PRINTS; PR00019; LEURICR1.F.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 KW Glycoprotein; Immune response; Inflammatory response; Innate immunity;
 KW Leucine-rich repeat; Membrane; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 31 Potential.
 FT CHAIN 32 796 TOLL-like receptor 6.
 FT FT FT /FTid=PRO_0000034731.
 FT TRANSDOM 32 586 Extracellular (Potential).
 FT FT 587 607 Potential.
 FT TOPO_DOM 608 796 Cytoplasmic (Potential).
 FT REPEAT 51 74 LRR 1.
 FT REPEAT 75 98 LRR 2.
 FT REPEAT 100 120 LRR 3.
 FT REPEAT 121 144 LRR 4.
 FT REPEAT 158 175 LRR 5.
 FT REPEAT 176 201 LRR 6.
 FT REPEAT 222 248 LRR 7.
 FT REPEAT 376 400 LRR 8.
 FT REPEAT 402 428 LRR 9.
 FT REPEAT 430 447 LRR 10.
 FT REPEAT 449 472 LRR 11.
 FT REPEAT 474 496 LRR 12.
 FT REPEAT 498 517 LRR 13.
 FT DOMAIN 640 784 TIR.
 FT CARBOHYD 144 144 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 186 186 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 214 214 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 253 253 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 285 285 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 359 359 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 423 423 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 434 434 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 583 583 N-linked (GlcNAc . . .) (Potential).
 SQ SEQUENCE 796 AA; 91890 MM; 35CFAEC05BFBAB8D CRC64;

Query Match 99.9%; Score 4149; DB 1; Length 796;
 Best Local Similarity 99.9%; Pred. No. 8e-251;
 Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDKKEPIVKSHPFCVIMIIIVGTRIQPSDGNFPAIDKRGILHYPKDPLKTKYLDWS 60
 DB 1 MKDKKEPIVKSHPFCVIMIIIVGTRIQPSDGNFPAIDKRGILHYPKDPLKTKYLDWS 60

QY 61 QNYIAELQVSDMSFLSELTVLRLSHNRIQLIDLSVFEKNODLEYLDLSHNOLOKISCHPI 120
 DB 61 QNYIAELQVSDMSFLSELTVLRLSHNRIQLIDLSVFEKNODLEYLDLSHNOLOKISCHPI 120
 QY 121 VSPFRLDLSFNDPFLALPCKEFGNLSQNLNPLGLSAMLKQKDLPIAHILHLSYLLDLRN 180
 DB 121 VSPFRLDLSFNDPFLALPCKEFGNLSQNLNPLGLSAMLKQKDLPIAHILHLSYLLDLRN 180
 QY 181 YIKENETESQIINAKTLHLVFHPTSLFAIQVNI SVNTLGLQTLNIKNDNCQVFIK 240
 DB 181 YIKENETESQIINAKTLHLVFHPTSLFAIQVNI SVNTLGLQTLNIKNDNCQVFIK 240
 QY 241 FLSELTRGSLTNLTNLHIEFTWKCLVRFQFLMPKPEVEYININLTIESIREDFYIS 300
 DB 241 FLSELTRGSLTNLTNLHIEFTWKCLVRFQFLMPKPEVEYININLTIESIREDFYIS 300
 QY 301 KTLTKALTEHTTNOVFLFQSTALYTVFSENNIMMLTISDPFTHMLCPHAPSTFKPLNF 360
 DB 301 KTLTKALTEHTTNOVFLFQSTALYTVFSENNIMMLTISDPFTHMLCPHAPSTFKPLNF 360
 QY 361 TONVFTDSIFPKCSTLYVLETLILQKGLKDLFFVGLMTKDPSELIDVSMNSLBSGRH 420
 DB 361 TONVFTDSIFPKCSTLYVLETLILQKGLKDLFFVGLMTKDPSELIDVSMNSLBSGRH 420
 QY 421 KENCTWVESIVLNLSSNMLTDSVFRCLPPIKXVLDHSNKIKSVKQVVKLEALQELNV 480
 DB 421 KENCTWVESIVLNLSSNMLTDSVFRCLPPIKXVLDHSNKIKSVKQVVKLEALQELNV 480
 QY 481 AFNSLTDLPGGSSPSLVLLIDHNSVSPADPFQSCQKRSIKAGDNPCQCELEEF 540
 DB 481 AFNSLTDLPGGSSPSLVLLIDHNSVSPADPFQSCQKRSIKAGDNPCQCELEEF 540
 QY 541 VNIDQVSSEVLLEGMPDSYKCDYPSYKSPDKDFHMSLSCNTLLIVTIGATMLVLAV 600
 DB 541 VNIDQVSSEVLLEGMPDSYKCDYPSYKSPDKDFHMSLSCNTLLIVTIGATMLVLAV 600
 QY 601 TVTSICILYLDLPWYIRMYCQOTRRRARNIPLELOLNLOPHAFISSEHDSAMVSEL 660
 DB 601 TVTSICILYLDLPWYIRMYCQOTRRRARNIPLELOLNLOPHAFISSEHDSAMVSEL 660
 QY 661 VPELEKEDIQCLHERNVPGKSIYENTINCIEKSYKSIFFLSPNFVQSEKCHELYFAH 720
 DB 661 VPELEKEDIQCLHERNVPGKSIYENTINCIEKSYKSIFFLSPNFVQSEKCHELYFAH 720
 QY 721 HNLFFEGSNMILILILEPIPNKSYKUKLALMTORTYLOMPKSKRGIFMANIRAA 780
 DB 721 HNLFFEGSNMILILILEPIPNKSYKUKLALMTORTYLOMPKSKRGIFMANIRAA 780
 QY 781 FNMKLTVTENNDDVKS 796
 DB 781 FNMKLTVTENNDDVKS 796

RESULT 2
 ID 059HI6_PIG PRELIMINARY; PRT; 796 AA.
 AC 059HI6;
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 26-APR-2005, sequence version 1.
 DE TOLL-like receptor 6.
 GN Name=TLR6;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OC NCB1_TaxID=9823;
 RN NUCLEOTIDE SEQUENCE.
 RP Shikai H., Uenishi H.;
 RT "Coding sequence of porcine TLR6";
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 [2]

RP NUCLEOTIDE SEQUENCE.
RA Shinkai H., Uenishi H.;
RT "Nucleotide sequence of porcine genomic region containing TLR1, TLR6
RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL, AB208698; BAD91801.1; -; Genomic DNA.
DR EMBL, AB210286; BAD93713.1; -; Genomic DNA.
DR SMR, Q59H16; 630-785.
DR GO, GO:0016020; C:membrane; IEA.
DR GO, GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro, IPR004075; IIL_rcpt_1.
DR InterPro, IPR001611; LRR.
DR InterPro, IPR00483; LRR_C.
DR InterPro, IPR003591; LRR_Typ.
DR InterPro, IPR000157; TIR.
DR Pfam, PF00560; LRR_1; 7.
DR Pfam, PF01463; LRRCT; 1.
DR Pfam, PF01582; TIR; 1.
DR PRINTS, PR01537; INTRLNRI1.F.
DR PRINTS, PR00019; LEURICRPT.
DR SMART, SM00082; LRRCT; 1.
DR SMART, SM00255; TIR; 1.
DR PROSITE, PS50104; TIR; 1.
KM Receptor.
SQ SEQUENCE 796 AA; 91460 MW; 8CE2A2375606CA55 CRC64;

Query Match 81.2%; Score 3374; DB 2; Length 796;
Best Local Similarity 79.4%; Pred. No. 2,4e-202;
Matches 632; Conservative 77; Mismatches 87; Indels 0; Gaps 0;

QY 1 MTKDKEPIVKSFFHYCLMIIIVGTRIQPSDGNFAVDKSKRGLHVPKDLPIKTVLDM 60
DB 1 MSKDKEPIVISHSYVMTLVWGTLIQFSESEFVVDKSKGLTRVPKDLPTQTVLDM 60
QY 61 QNYIAELQVSDMSFLSELTVLRSLSHNRIOQLDLVSFKENODLEVLDSLNOLOKISCHPI 120
DB 61 QNFITELHLSIDISFSLQTLVRLSQNRMOCLDISVFKFNODLEVLDSLNOLOKISCHPI 120
QY 121 VSPFRLDSFNDFKALPICKEFGNLSQNLFLGLSAMKLOKLDLPIAHMLSYILLDLN 180
DB 121 TSLKRLDSFNDFKALPICKEFGNLTQNLFLGLSATKLOQDLPLPAHMLSCILLDLN 180
QY 181 YYIKENETESQIOLNAKTLHLVHPSTSLPAIGVNISVNTLGLQOLTNIKLNDNCQVPIK 240
DB 181 YYMKENETESQIOLNMTKHLVHPNSPFSVGVNISVSVGLQLANIKLSDNCQVPIK 240
QY 241 FLSELTGRSTLINFTLNHETWKCLVRFQFLMKPEVLEYINYLTIESTIREDFYIS 300
DB 241 FLLELTQGPFTLINFTLNHETWKCLVGFQFLMKPEVLEYINYLTIESTIREDFYIY 300
QY 301 KTTLKALTIENHTNQVFLFSOTALTVPSENNIMMLTSDPFIHMLCPHASTKPLNF 360
DB 301 ETTLKGVKTIENHTKRVFLFSOTALTVPSENNIMMLTSDPFIHMLCQVSTNPLNF 360
QY 361 TQNVFTDSIFPKCSTLVKLETLILQKNGIKDLFKVGLMTKMDPSLEILDVSNWSSEGRH 420
DB 361 TQNVFTDSVFQCKTLARLETLILQKMKLEDFKISLMTKMDLSLEILDVSNWSSEGRH 420
QY 421 KENCWVSGIYVLANSSNMULTSVPRCLPPIKATLDLSHNKTKSPKQVYKLEALQELNV 480
DB 421 GENCWVSGIYVLANSSNMULTSVPRCLPPIKATLDLSHNKTKSPKQVYKLEALQELNV 480
QY 481 AFNSTLTDIPGCGSFESLSTLIDHNSVSHPSADFPQSCOKMSIRAGNDPFOCTCELRIF 540
DB 481 ASNSTLTDIPGCGSFESLSTLIDHNSVSHPSADFPQSCOKMSIRAGNDPFOCTCELRIF 540
QY 541 VKNIDQVSSVLEGMPSDYKCDYPESYRSGPLKDPHMSLSCNTLLITVITATMLVLAV 600
DB 541 IQSLQVSSDVVLEGMPSDYKCDYPESYRSGPLKDPHMSLSCNTLLITVITATMLVLAV 600

QY 601 TWTSLICILYDLPWYLRMVCOMWOTRRRARNPIPLEIQRNLQPHAFISYSEHDSANVKSRL 660
DB 601 TWTGLCVFDFLPWYLRLMCOMWOTRRRARNPIPLEIQRNLQPHAFISYSEHDSANVKSRL 660
QY 661 VPLYEKEDIQICLHERNFVPGKSIYENIINCIEKYSKISFVLSPNFVQSEWCHYELYPFH 720
DB 661 VPLYEKEDIQICLHERNFVPGKSIYENIINCIEKYSKISFVLSPNFVQSEWCHYELYPFH 720
QY 721 HNLFFHESGNNLILILLEPDPNSIPNKYHKLKALMTOSTYLOMPKEKSKRGLFWANIRAA 780
DB 721 HNLFFHESGNNLILILLEPDPNSIPNKYHKLKALMAORTYLBWPEKSKRGLFWANIRAA 780
QY 781 FNMKRLTVLENNDVKS 796
DB 781 FNMKRLTVLENNDVKT 796

RESULT 3
ID 076L23_PIG PRELIMINARY; PRT; 796 AA.
AC 076L23;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Toll-like receptor 6.
GN Name=TLR-6;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22948431; PubMed=14585198; DOI=10.1089/107999003322485080;
RA Muneta Y., Uenishi H., Kikuma R., Yoshihara K., Shimoji Y.,
RA Yamamoto R., Hamashina N., Yokomizo Y., Mori Y.;
RT "Porcine TLR2 and TLR6: identification and their involvement in
RT Mycoplasma hyopneumoniae infection."
RL J. Interferon Cytokine Res. 23:583-590(2003).
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CC -----
CC EMBL, AB085936; BAC99317.1; -; mRNA.
DR SMR, Q76L23; 630-785.
DR GO, GO:0016020; C:membrane; IEA.
DR GO, GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro, IPR004075; IIL_rcpt_1.
DR InterPro, IPR001611; LRR.
DR InterPro, IPR000483; LRR_C.
DR InterPro, IPR003591; LRR_Typ.
DR InterPro, IPR000157; TIR.
DR Pfam, PF00560; LRR_1; 7.
DR Pfam, PF01463; LRRCT; 1.
DR Pfam, PF01582; TIR; 1.
DR PRINTS, PR01537; INTRLNRI1.F.
DR PRINTS, PR00019; LEURICRPT.
DR SMART, SM00082; LRRCT; 1.
DR SMART, SM00255; TIR; 1.
DR PROSITE, PS50104; TIR; 1.
KM Receptor.
SQ SEQUENCE 796 AA; 91414 MW; 36C489D2CC339F81 CRC64;

Query Match 80.9%; Score 3361; DB 2; Length 796;
Best Local Similarity 79.1%; Pred. No. 1.6e-201;
Matches 630; Conservative 77; Mismatches 89; Indels 0; Gaps 0;

QY 1 MTKDKEPIVKSFFHYCLMIIIVGTRIQPSDGNFAVDKSKRGLHVPKDLPIKTVLDM 60
DB 1 MTKDKEPIVISHSYVMTLVWGTLIQFSESEFVVDKSKGLTRVPKDLPTQTVLDM 60
QY 61 QNYIAELQVSDMSFLSELTVLRSLSHNRIOQLDLVSFKENODLEVLDSLNOLOKISCHPI 120

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Db      61 QNFITELHLSDISFSLQTLVRLSONRMOCLDISVEKFNODLEYLDLSHNOLOTLICHP1 120
Qy      121 VSPFRLDLSFNDPKFLPICKEFGNLSQNLFLGSLAMKLOKDLPLIAHLHSYILLDRN 180
Db      121 TSLKHLDSFNDPKFLPICKEFGNLTQNLFLGSLATKLOQDLPLIAHLHSYILLDR 180
Qy      181 YYIKENETESLOILNAKTLHLVHPPTSLFAIOVNI SVNTLGLQLTNKLKNDNCQVFLK 240
Db      181 YYMKENEKESLOILNTEKHLVHPHNSFFSVQVNI SVKSVGLQLANIKLGDNCQVFLT 240
Qy      241 FLSELTTRSTLNLPLNLNIETTWKCLVAFQFLMKPEVEYLNINYULTIIESREEDFTYS 300
Db      241 FLEELTQGPPLNLPLNLNVEITWKCLVGFQFLMKPEVEYLSIYNLTIVESIDEDPFIY 300
Qy      301 KTYLKALTEHITNOVPLFSCOTALTVESENNIMLTISDTEFIHMLCPHASTKFLNLF 360
Db      301 ETTLKGVKLEHTKVFIFSQALYRVSDNNIRMLTADTFIIMLCFQVSTENFLNLF 360
Qy      361 TQNVFTDSIFEKCSLTVKLETLILQKNGKLDLFFKGLMTKMPSLLEILDVSNLSBSGR 420
Db      361 TQNVFTDSVFQCKTLARLETLILQKNGKLEDLFXISMTKMDLSLEILDVSNLSBYDR 420
Qy      421 KENCTWVESIYVNLSSNNLTDVFRCLPFRITKVIDLHSNKTKSVPKQYVKLBALQELNV 480
Db      421 GENCTWVGSIYVNLSSNLTDSVFRCLPFRITKVIDLHSNRIRISIPKDVANLEALQELNV 480
Qy      481 AFNLSITDLPGGCSFESLTVLIIIDHNSVSHSPADFPQSCOKMSIRKAGNPPQCTGELREF 540
Db      481 ASNSIAHLPGGCSFESLSLISIDVNSISNPSADFPQSCOKIRSLKAGNPPQCTGELNDF 540
Qy      541 VKNIDQVSSEVLGMPDPSYKCDYPSYSGSPKCDPFHMSLSGNITLLITVIGATMLVLAV 600
Db      541 IQSGQVSSDVESMPDSYBCEYSGYKGLDKFRVSELSCNTALLITIGVGTALAL 600
Qy      601 TVTSLCTIYLDLPWYLRVWCQWQTRRRARNIPLELQNLQTHATISYSEHDSAVYKSEL 660
Db      601 TMTGLCVYFDLPWYLRVWCQWQTRRRARNIPLELQTHATISYSEHDSAVYKSEL 660
Qy      661 VPYLEKEIOICLHERNFPGKSIYVENIINCEKSYKSI FVLSPNVQSEWCHYELVYFAH 720
Db      661 VPCLKEBGKICLHERNFPGKSIYVENIINCEKSYKSI FVLSPNVQSEWCHYELVYFAH 720
Qy      721 HNLFEHSGNNLILILLEPIPNQSI PNKYHKLKALMTORTYLOMPKESKRGHFWANIRAA 780
Db      721 HNLFEHSGNNLILILLEPIPNQSI PNKYHKLKALMAQRTYLEMPKESKRGHFWANIRAA 780
Qy      781 FNMKLTLTENNVDKS 796
Db      781 FNIKLTVAEEDVDKT 796

RESULT 4
Q704V6_BOVIN PRELIMINARY, PRT, 793 AA.
AC Q704V6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Toll-like receptor 6.
GN Name=tlr6;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yang W., Weikard R., Zerhe H., Seyfert H.M.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AJ620670; CAF06197.1; -; Genomic DNA.
DR SMR; Q704V6; 630-789.
DR Ensemble; ENSBTAG00000014031; Bos taurus.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR004075; IIL_rcpt_1.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003591; LRR_TYP.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR_1; 7.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR01537; INTRLNLR1F.
DR PRINTS; PR00019; LEURICRPT.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS0104; TIR; 1.
DR KX Receptor.
SQ SEQUENCE 793 AA; 90927 MW; C11C26099F8E3668 CRC64;

Query Match          79.8%; Score 3315; DB 2; Length 793;
Beet Local Similarity 79.5%; Pred. No. 1.2e-198;
Matches 625; Conservative 73; Mismatches 86; Indels 2; Gaps 2;

1  MTKDEPIVKSFFHFCMLIIIVGTRIQPSDGNFPAVDSKRGKGLIHVPKDLPLKTVLDM 60
Db  1  MIKDESPIRSCHFYIYALVFGTIIQFSDSEFVDMSKSLIHVPKDLPLKTVLDM 60
Qy  61  QNYIAELQVSDMPSLSELTVLRLSHNRIQILDVYFKNODLEYLDLSHNOLOKISCHPI 120
Db  61  QNNISELHLSDISFSLGRLVRLSHNRIOGLDISIFKFNHLEYLDLSHNOLOKISCHPI 120
Qy  121 -VSFRHLDSFNDPKFLPICKEFGNLSQNLFLGSLAMKLOKDLPLIAHLHSYILLDR 179
Db  121 TTYLKHLDLSFNDPKFLPICKEFGNLQNLFLGSLATKLOQDLPLIAHLHSYILLDR 180
Qy  180 NYIYIKENETESLOILNAKTLHLVHPPTSLFAIOVNI SVNTLGLQLTNKLKNDNCQVFI 239
Db  181 D-YMKENEKESLOILNTEKHLVHPHNSFFSVQVNI SVKSVGLQLANIKLGDNCQVFL 239
Qy  240 KFLSELTTRSTLNLPLNLNIETTWKCLVAFQFLMKPEVEYLNINYULTIIESREEDFTY 299
Db  240 KFLSGLTGPPPLNLPLNLNVEITWKCLVGFQFLMKPEVEYLNINYULTIIVESIDEDPFIY 299
Qy  300 SKTYLKALTEHITNOVPLFSCOTALTVESENNIMLTISDTEFIHMLCPHASTKFLNLF 359
Db  300 KYTLKALKLEHTKVFIFSQALYRVSDNNIRMLTADTFIIMLCFQVSTENFLNLF 359
Qy  360 FTQNVFTDSIFEKCSLTVKLETLILQKNGKLDLFFKGLMTKMPSLLEILDVSNLSBSGR 419
Db  360 FTQNSFTDSVFQCKTLARLETLILQKNGKLEDLFXISMTKMDLSLEILDVSNLSBYDR 419
Qy  420 HKNCTWVESIYVNLSSNNLTDVFRCLPFRITKVIDLHSNKTKSVPKQYVKLBALQELNV 479
Db  420 SNGNSCWGSIYVNLSSNLTDSVFRCLPFRITKVIDLHSNRIRISIPKDVANLEALQELNV 479
Qy  480 VAFNLSITDLPGGCSFESLTVLIIIDHNSVSHSPADFPQSCOKMSIRKAGNPPQCTGELREF 539
Db  480 LASNSIAHLPGGCSFESLSLISIDVNSISNPSADFPQSCOKIRSLKAGNPPQCTGELNDF 539
Qy  540 FVKNIDQVSSEVLGMPDPSYKCDYPSYSGSPKCDPFHMSLSGNITLLITVIGATMLVLAV 599
Db  540 FIQSGQVSSDVESMPDSYKCDYPSYSGSPKCDPFHMSLSGNITLLITVIGATMLVLAV 599
Qy  600 VVTVSLCTIYLDLPWYLRVWCQWQTRRRARNIPLELQNLQTHATISYSEHDSAVYKSEL 659
Db  600 VAVTVLCTIYLDLPWYLRVWCQWQTRRRARNIPLELQTHATISYSEHDSAVYKSEL 659
Qy  660 LVPLYLEKEDIOICLHERNFPGKSIYVENIINCEKSYKSI FVLSPNVQSEWCHYELVYFA 719
Db  660 LIPNLEKEDIRICLHERNFPGKSIYVENIINCEKSYKSI FVLSPNVQSEWCHYELVYFA 719

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OY	720	HNNLHFGSSNNLILILTEEPONSIENKCHKUKALMTORTYLOMPKEKSRGGFWANNIRA	779
DB	720	HNNLHFGSSNNLILILDELPOTIPSSYHKULNALMAORTLYEMPEKSRGHLFWANNIRA	779
OY	780	AFNMKL 785	
DB	780	SINIKL 785	
RESULT 5			
ID	Q706D2	BOVIN	PRELIMINARY; PRT; 793 AA.
AC	Q706D2		
DT	05-JUL-2004		Integrated into UniProtKB/TrEMBL.
DT	05-JUL-2004		Sequence version 1.
DT	07-FEB-2006		entry version 12.
DE	Toll-like receptor 6.		
GN	Name=tlr6;		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;		
OC	Pecora; Bovidae; Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Mammary gland.		
RA	Yang W., Weikard R., Zeide H., Seyfert H.M.,		
RL	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Weirung D.;		
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.		
CC	-----		
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CC	-----		
DR	EMBL; AJ618974; CAP02015.1; -; mRNA.		
DR	EMBL; AY487803; AAY40896.1; -; mRNA.		
DR	Ensembl; ENSBTAG00000014031; Bos taurus.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:004888; F:transmembrane receptor activity; IEA.		
DR	InterPro; IPR004075; IL1_rcpt_1.		
DR	InterPro; IPR001611; LRR_		
DR	InterPro; IPR004833; LRR_C.		
DR	InterPro; IPR003591; LRR_1yp.		
DR	InterPro; IPR001573; TIR.		
DR	Pfam; PF00560; LRR_1; 7.		
DR	Pfam; PF01463; LRRCT; 1.		
DR	Pfam; PF01582; TIR; 1.		
DR	PRINTS; PRO1537; INTRLNKLRP.		
DR	PRINTS; PRO0019; LEURICHRPT.		
DR	SMART; SM00082; LRRCT; 1.		
DR	SMART; SM00255; TIR; 1.		
DR	PROSITE; PSS0104; TIR; 1.		
KW	Receptor.		
SO	SEQUENCE		
	793 AA, 90927 MW, D52422389B09F28F CRC64;		
Query Match 79.6%; Score 3306; DB 2; Length 793;			
Best Local Similarity 79.4%; Pred. No. 4,3e-198;			
Matches 624; Conservative 73; Mismatches 87; Indels 2; Gaps 2			
OY	1	MTKDKDEPIVSKSHFPCIMIIIVGTRIOFSDNGNEFAVDKSRGILHVPKDLPLTKTIDMS	60
DB	1	MTKDKESPIRSHCFYIYALVFGITIIQFSDSEFVDMSTSLIHVPKDLPPPTKVLIDS	60
OY	61	QNTYIAELQVDSNFSFSELTVLRLSHNRIQLDLVFEKFNQDLEYYLDLSHNQLOKISCHPI	120
DB	61	QNNISLEHLSDISFISGLKVLRLSHNRIGGLDLSIFKFNHDEYLDLSHNQLOKISCHPI	120
OY	121	VSPFHLDSFNDKALPLCKKFGNLSQNLNFGLSAMKLOKQDLPLPIALHLSTYILLDR	179
DB	121	VSPFHLDSFNDKALPLCKKFGNLSQNLNFGLSAMKLOKQDLPLPIALHLSTYILLDR	179

Db	121	TTTTLKHLDLSPDFPALP	CKEFGNLTQCNLFGLSATKQGDLDLP	IAHLHLSCLLDE	180				
Qy	180	NYIKENENESIQIINAKT	LHLVHPPTSLFAIQVNISVNTLGCLOT	TNIRKANDNCQVFI	239				
Db	181	D-YMKENKESIQIINTKT	LHLVHPHNSFFQVVDISGNSLACLQ	TNIRKANDYCNVL	239				
Qy	240	KFLSLTSGSTLNTANT	LHIEFTTWKCVAVPQFIMPKPREYIN	YNLTIIESIREDFTY	239				
Db	240	KFLSGLTGGPFLNTL	NHVEFTTWKCLVAVQFQFLMPKPLEY	INYNLTIIVESIDEDEFTY	239				
Qy	300	SKTTLKALTIIEHTIQ	OVLFESQTAIYVFSENNIML	TTISDPFIHMLCPHASTFEFLN	355				
Db	300	YKTIKALKIIEHTTKV	PIFQSOTAIYVSENNIIML	TTISDRFIHMLCPQESTKFLN	355				
Qy	360	FTQNVFTDSIEFKS	CTVYKLETLIIQKGLKDL	PKVGLMTKMPSLIILDVSNLSISGR	419				
Db	360	FTQNSFTDSVPQNC	TTLARLETLIIQKELKDL	PKTSIMTKMLSLIETLIDVSNLSIDYR	419				
Qy	420	HKENCTWBSIYVNL	SSNMLTDSVPRCLP	PRIKYLDLHNSKIKSPKQVVKLEAQELN	479				
Db	420	SNGNSWGSIVVNL	SSNALTDSVPRCLP	PRIKYLDLHNNRIRSI	PKDVTGLETIQEIN	479			
Qy	480	VAFNSLTDLPGGSS	SSLVLIIDHNSVSHPADP	FQSCQKRSIRKAGNPFQCTGELRE	539				
Db	480	IANSNLHLPGGCIR	ISSUSILIEHNSISNPAD	PFQSCQKRSIRLAGNPPQSCGELRD	539				
Qy	540	FVKNIIDVSSSELT	BEGMPDSYKCDYESYSGSLPK	DFHMSLSCNTLLITVIGATMLVLA	599				
Db	540	FIQSGQGVSSDVE	BEMPESYKCDYESYSGTLP	KQFQVSELSCNTALLIITIVVGLVLA	599				
Qy	600	VTVISLCIYLDL	PWLYRMVCOMTORRRARNI	PBELQNLQFHAFISYSEHDSAVKSE	659				
Db	600	VAVTVLCIYLDL	PWLYRMVCOMTORRRARNI	PBELQRTILOFHAFISYSEHDSAVKNE	659				
Qy	660	LVPYLEKDKIOI	CHERNVPVSKSI	IVENINICIEKSYKSI	FIYLSPPVQSEWCHYELVYA	719			
Db	660	LIPNEKEDIRI	CHERNVPVAKS	IVENINICIEKSYKSI	FALSPFVQSEWCHYELVYA	719			
Qy	720	HHNLPHESNNML	ILILPEIPONSIPNKYHK	KALMTORTYQWPREKSKRGFLFMANIRA	779				
Db	720	HHNLPHESDNL	ILILDLPIPYSIPSSHKL	RALMAQRTTYLEWPREKSKRGHGFMANLRA	779				
Qy	780	AFNMKL	785	:					
Db	780	SINIKL	785	:					
RESULT 6									
AC	06P690	RAT	PRELIMINARY;	PRT;	806 AA.				
DT	05-JUL-2004	integrated into UniProtKB/TrEMBL.							
DT	07-FEB-2006	entry version 12.							
DE	Toll-like receptor 6.								
GN	Name=Tlr6;								
OS	Rattus norvegicus (Rat).								
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;								
OC	Muroidea; Muridae; Murinae; Rattus.								
OX	NCBI_TaxID=10116;	[1]							
RP	NUCLEOTIDE SEQUENCE.								
RC	TISSUE=Prostate;								
RX	MEDLINE=2238957;	PubMed=12477932. DOI=10.1073/pnae.242603899;							
RA	Straussberg R.U., Feingold E.A., Grouse L.H., Dege J.G.,								
RA	Klausner R.D., Collins F.S., Wagner L., Schenel C.M., Schuler G.D.,								
RA	Altschul S.F., Zeeberg B., Bueckow K.H., Schaefer C.F., Bhat N.K.,								
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,								
RA	Diatchenko L., Murusina K., Farmer A.A., Rubin G.M., Hong L.,								
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,								
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,								
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,								

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Bikesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Prostate;
 RA Director MGC Project;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: BC062390; AA062390.1; -; mRNA.
 DR SMR; Q6P690; 641-796.
 DR Ensembl; ENSRNOG00000002161; Rattus norvegicus.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR004075; IL1 rcpt_1.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_C.
 DR InterPro; IPR003591; LRR_Typ.
 DR Pfam; PF00560; LRR_1; 8.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PRO1537; INTRLNKLRP.
 DR PRINTS; PRO0019; LEURICRPT.
 DR SMART; SM00369; LRR_Typ; 1.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS0104; TIR; 1.
 KM Receptor.
 SQ SEQUENCE 806 AA; 92567 MW; F157P9D6447DAF3A CRC64;
 Query Match 75.8%; Score 3147.5; DB 2; Length 806;
 Best Local Similarity 74.2%; Pred. No. 3.6e-188;
 Matches 591; Conservative 91; Mismatches 113; Indels 1; Gaps 1;
 QY 1 MTKDEPIYKSPHYVCLMIIIVGTRIQSPDGNFPAVDKSKRGLIHVPKDLPLTKYLDMS 60
 DB 12 MSQDEPIYKSPHYVCLMIIIVGTRIQSPDGNFPAVDKSKRGLIHVPKDLPLTKYLDMS 71
 QY 61 ONYIAELOVDMSPISELTVLRSLSHNRIOQLDLSVFKPNQDLEVDYLDISNOLOKTSCHPI 120
 DB 72 ONISIDLOVMSDPISELTVLRSLSHNRIRRLDGFVLLRLDLEVDVSHNOLOKTSCHPI 131
 QY 121 VSFRLDLSFNDPKALPICKEFGNLSQNLFLGLSANKLOKLLPLAHHLVYLLDLRN 180
 DB 132 VNLKRLDLSFNDPKALPICKEFGNLSQNLFLGLSANKLOKLLPLAHHLVYLLDLRN 191
 QY 181 YYIKENETESQILNAKTLHLVPHPTSLFAIOVNISVNTLGLQLTNIKLANDNCQVPIK 240
 DB 192 YQIKGEETESQILNAKTLHLVPHPTSLFAIOVNISVNTLGLQLTNIKLANDNCQVPIK 251
 QY 241 FLSELTSTLNLNLNLTNHTETTKCLVRFOGLMPDPVYLYNLTITESTREDFPMYS 300
 DB 252 FLSELTSTLNLNLNLTNHTETTKCLVRFOGLMPDPVYLYNLTITESTREDFPMYS 311
 QY 301 KTKLALTEHTITNOVFLFSOTALYTVFSENNIMMLTISDPPIHMLCPHASTFEKFLNF 360
 DB 312 ETVLKSLEKTEHTITNOVFLFSOTALYTVFSENNIMMLTISDPPIHMLCPHASTFEKFLNF 371
 QY 361 TQNVFTDSIFEKCSLTIVKLETLILQKNGKDLFKVGLMTKMPSLSEILDVSNMSLESGRH 420

DB 372 TQNVFTDSIFQGCSTLVKLETLILQKNGKDLFKVGLMTKMTSLSEILDVSNMSINSVY 431
 QY 421 KENCTWVESIVLNLSSNMLTDSVFCRPPRIKYLDLSHNKIKSPKOVKLEALOELNV 480
 DB 432 DRTCMASIRVNLSSNMLTDSVFCRPPRIKYLDLSHNKIKSPKOVKLEALOELNV 491
 QY 481 AFNSTIDLPGCCGSPSSLSVLIIDHNSVSHPADFPQSCQKRSIYAGNPQCTCELEEF 540
 DB 492 ASNFLTIDLPGCCGSPSSLSVLIIDHNSVSHPADFPQSCQKRSIYAGNPQCTCELEEF 551
 QY 541 VKNIDQVSEVLEGGPDSPKDYSPESYSGSLPKDPHMSLSCNTLLIVTTGATMYLAV 600
 DB 552 VKNIDQVSEVLEGGPDSPKDYSPESYSGSLPKDPHMSLSCNTLLIVTTGATMYLAV 611
 QY 601 TYSLSICLYLDLPWYLRWVCOMTQTRRARNPIPLELOQNLQPHAFISYSEHDSAVKSEL 660
 DB 612 IGASLCILYLDLPWYLRWVCOMTQTRRARNPIPLELOQNLQPHAFISYSEHDSAVKSEL 671
 QY 661 VPELEKEDIQICLHERNFVPGKSIYENIINCIEKYSKIFVLSNPFVQSEWCHIELYFAH 720
 DB 672 LPNLEKDDIRVCLHERNFVPGKSIYENIINIEKYSKIFVLSNPFVQSEWCHIELYFAH 731
 QY 721 HNLFRGSSNMLIILIEPIPNQSI PNKYHKLKALMTORTYLOMPKSKRGLFWANIRAA 780
 DB 732 HNLFRGSSNMLIILIEPIPNQSI PNKYHKLKALMTORTYLOMPKSKRGLFWANIRAA 791
 QY 781 FNMKRLTVLTENNVDYS 796
 DB 792 FNMKRLTVLTENNVDYS 806
 RESULT 7
 ID TIR6 MOUSE STANDARD; PRT; 795 AA.
 AC O9EB99; O9WT04; Integrated into UniProtKB/Swiss-Prot.
 DT 31-JAN-2002, sequence version 2.
 DT 07-MAR-2006, entry version 40.
 DE Toll-like receptor 6 precursor.
 GN Name=TLR6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Embryo;
 RX MEDLINE=99250250; PubMed=10231569; DOI=10.1016/S0378-1119(99)00098-0;
 RA Takeuchi O., Kawai T., Sanjo H., Copeland N.G., Gilbert D.J.,
 RA Jenkins N.A., Takeda K., Akira S.,
 RT "TLR6: a novel member of an expanding Toll-like receptor family.";
 RL Gene 231:59-65(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND MUTAGENESIS OF PRO-680.
 RC STRAIN=BALB/c; TISSUE=Macrophage;
 RX MEDLINE=2058581; PubMed=11095740; DOI=10.1073/pnas.250476497;
 RA Ozolsky A., Underhill D.M., Fontenot J.D., Hajjar A.M., Smith K.D.,
 RA Wilson C.B., Schroeder L., Aderem A.;
 RT "The repertoire for pattern recognition of pathogens by the innate
 RT immune system is defined by cooperation between Toll-like receptors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:13766-13771(2000).
 CC -!- FUNCTION: Participates in the innate immune response to Gram-
 CC positive bacteria and fungi. Acts via MyD88 and TRAF6, leading to
 CC NF-kappa-B activation, cytokine secretion and the inflammatory
 CC response. Cooperates with TLR2 for the cellular activation (By
 CC similarity).
 CC -!- SUBUNIT: Binds TLR2 via their respective extracellular domains.
 CC Binds MyD88 via their respective TIR domains (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
 CC phagosomes.
 CC -!- TISSUE SPECIFICITY: Detected in thymus, spleen, ovary and lung.
 CC -!- SIMILARITY: Belongs to the Toll-like receptor family.

	-	SIMILARITY:	Contains 14 LRR(leucine-rich) repeats.
CC	-	SIMILARITY:	Contains 1 TIR domain.
CC	-	SIMILARITY:	-----
CC	Copied	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	
CC	Distributed under the Creative Commons Attribution-NoDerivs License		
CC	EMBL; AB078906; BAA78632.1; ALT_INIT; mRNA.		
DR	EMBL; AF314636; AAG38563.1; ALT_INIT; mRNA.		
DR	HSSP; Q15399; IEFV.		
DR	SMR; O9EPW9; 630-785.		
DR	Ensembl; ENSMUSG0000051498; Mus musculus.		
DR	MGI; MGI:1341296; Tir6.		
DR	GO; GO:0016021; C:integral to membrane; TAS.		
DR	GO; GO:0016020; C:membrane; ISS.		
DR	GO; GO:0045335; C:phagocytic vesicle; ISS.		
DR	GO; GO:0008034; F:lipoprotein binding; IMP.		
DR	GO; GO:0004888; F:transmembrane receptor activity; ISS.		
DR	GO; GO:0007280; P:activation of NF-kappaB-inducing kinase; ISS.		
DR	GO; GO:0009598; P:detection of pathogenic bacteria; ISS.		
DR	GO; GO:0042116; P:macrophage activation; ISS.		
DR	GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . ; NAS		
DR	GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . ; ISS		
DR	GO; GO:0042088; P:T-helper 1 type immune response; IC.		
DR	InterPro; IPRO04075; IL1_rept_1.		
DR	InterPro; IPRO01611; LRR.		
DR	InterPro; IPRO00483; LRR_C.		
DR	InterPro; IPRO03591; LRR_TYP.		
DR	InterPro; IPRO00157; TIR.		
DR	Pfam; PF00560; LRR_1; 6.		
DR	Pfam; PF01463; LRRTT_1.		
DR	Pfam; PF01582; TIR; 1.		
DR	PRINTS; PRO1537; INTRLNRIAF.		
DR	PRINTS; PRO0019; LEURICRP.		
DR	SMART; SMO0369; LRR_TYP; 1.		
DR	SMART; SMO0082; LRRTT_1.		
DR	SMART; SMO0255; TIR; 1.		
KW	PROSITE; PS50104; TIR; 1.		
KW	Glycoprotein; Immune response; Inflammatory response; Innate immunity;		
KW	Leucine-rich repeat; Membrane; Receptor; Repeat; Signal;		
KW	Transmembrane.		
FT	SIGNAL	1	27 Potential.
FT	CHAIN	28	795 Toll-like receptor 6. /FtId=PRO_0000034732.
FT	TOPO_DOM	28	584 Extracellular (Potential).
FT	TRANSEM	585	605 Potential.
FT	TOPO_DOM	606	795 Cytoplasmic (potential).
FT	REPEAT	32	51 LRR 1.
FT	REPEAT	52	75 LRR 2.
FT	REPEAT	76	98 LRR 3.
FT	REPEAT	100	120 LRR 4.
FT	REPEAT	121	144 LRR 5.
FT	REPEAT	146	171 LRR 6.
FT	REPEAT	225	248 LRR 7.
FT	REPEAT	330	353 LRR 8.
FT	REPEAT	376	399 LRR 9.
FT	REPEAT	402	425 LRR 10.
FT	REPEAT	427	449 LRR 11.
FT	REPEAT	459	472 LRR 12.
FT	REPEAT	473	496 LRR 13.
FT	REPEAT	498	517 LRR 14.
FT	DOMAIN	640	784 TIR.
FT	CABOHYD	42	42 N-linked (GLCNAC. .) (Potential).
FT	CABOHYD	114	114 N-linked (GLCNAC. .) (Potential).
FT	CABOHYD	144	144 N-linked (GLCNAC. .) (Potential).
FT	CABOHYD	195	195 N-linked (GLCNAC. .) (Potential).
FT	CABOHYD	214	214 N-linked (GLCNAC. .) (Potential).
FT	CABOHYD	253	253 N-linked (GLCNAC. .) (Potential).
FT	CABOHYD	285	285 N-linked (GLCNAC. .) (Potential).
FT	CABOHYD	359	359 N-linked (GLCNAC. .) (Potential).
FT	CABOHYD	401	401 N-linked (GLCNAC. .) (Potential).
FT	CABOHYD	434	434 N-linked (GLCNAc. .) (Potential).
FT	MUTAGEN	680	p>H: Dominant negative mutant, blocks response to Gram-positive pathogens.

FT	CONFLICT	181	181	Y - H (in Ref. 1).					
SEQ	SEQUENCE	795 AA;	9116 MM;	34d84d2c33 CMC64;					
	Query Match	75.7%;	Score 3144.5;	DB 1;	Length 795;				
	Best Local Similarity	73.9%;	Pred. No. 5.4e-188;						
	Matches	588;	Conservative	97;	Mismatches 110; Indels 1; Gaps 1;				
QY		1	MTKQKEPIVSKFHHFYCLMTITVGRIRIQSDGNEFPVDSKXGGLHVPKDLPLKTKVLDMS	60					
DB		1	MSQPRKPIVSGFHHFCALALIVGSMTPSNELSESVADSNLTHVPKDLPLRTKALSLS	60					
QY		61	QNYIAELQVSMSPFSELTVLRLSHNRQLDLSVFKENQDLELYDLSHNOLOKISCHPI	120					
DB		61	QNSISELMPDISFSELRLVRLSHNRKRSIDFHFLEFLNQDLEYDLSHNRLONISCCPM	120					
QY		121	VSFRLHDSFPNDFALPICKFEGNLSQINFGLSAMKLOKIDLPIAHILSYILLDDRN	180					
DB		121	ASLRHLDSPNDFPVLVPCCKEFGNLTXTLTFGLSNAKFRQDLDPVAILHLSCHILLDVS	180					
QY		181	YYIKENETESLQIINAKTLHLVFHPTSLFAIQVNI SVNTGLCLOLTWIKINDDNCQVEIK	240					
DB		181	YHIKGGETESLQIPNTVTLVLFHPNSLSFQVNNMSVALGHLQLSNLIKNDENCCQRLMT	240					
QY		241	FLSELTRSTLNTLNTLNIETTWKCLVRPQWLPMPKPREYININLTIESIREDFEYS	300					
DB		241	FLSELTRPTLLNTLNTLOHIEETWKCQSVLRFQFMPRPAYEYININLTITERIDREEFYS	300					
QY		301	KTYLKALILEITNOVFLFSOTALATYVESNNIMMLTSDPFFHMLCPHAPSTPKFLNF	360					
DB		301	ETALKSLMIEHVAKQVFLFSKEALYSVFAENIKMLSDPFFHMCPEPSSFTFLNF	360					
QY		361	TQNVFTDSIFEKSGTLVYKLETLILQKGLKDLFFVGLMTKXMPSLBILDVSMNSLESGRH	420					
DB		361	TQNVFTDSVFGGSGTLKRLQTLILQKGLKDLFFVGLMTKXMSLETLDVSLNSHAY	420					
QY		421	KENCTWVESIVYVLLSSNMLTDSVFRCLPPIKXLDLSHNSKIKSVKPVQVYKLEALQELNV	480					
DB		421	DRTGAMESIIVYVLLSSNMLTGSVFRCLPPIKXLDLHNNRIMSI PKQVTHLOALQELNV	480					
QY		481	AFNSLTLDLPGGGSFSSVLIIIDHNSVHPADPFQSCQKRSIKAGNPQCCTELAEF	540					
DB		481	ASNSLTLDLPGGAFSSLSVLVLIIDHNSVHPEDPFQSQNTRSLLAGNPNPQCCTELAEF	540					
QY		541	VKNIDQVSEVLEEMPSPSKYCDPEBSYKGSPLKDFHMSSELSCNITLLITVIGATMLVAV	600					
DB		541	VKNIGWAVAREVEGMPDSYRCDPEBSKGTALRPFHMSPLSCDVLTLTIGATMLVAV	600					
QY		601	TVTSICLYLDLPMYLRVQCQMTQTRRRARNIPLBELQNLQFHAFLSYSEHDSAMVXSEL	660					
DB		601	TGAFCLCYFLDPMYVRMLCQMTQTRRRARHILPELQNLQFHAFLSVSEHDSAMVXNEL	660					
QY		661	VPLYLEKEDIQICLAEHRNFPVPGKSIYVENINICIEKSYSIFPLSRNPQOSEKCHLELYFAH	720					
DB		661	LPLNEKEDIQICLAEHRNFPVPGKSIYVENININIEKSYSAIFPLSHPIIOSEKCHLELYFAH	720					
QY		721	HNLFHEGSSNNLILILEPISONSIPNKYHKLKALMTORTYQWPKESKGLFVANIIRAA	780					
DB		721	HNLFHEGSSNNLILILEPILQNNIPSRYHKLRALMAQRTYLEMTEPKRGKGLFVANIIRAS	780					
QY		781	FNMKLITLVTENNDYKS	796					
DB		781	FIMKLTALVNE-DVYKT	795					
RESULT 8									
Q3UV88	MOUSE	PRELIMINARY;	PRT;	806	AA.				
AC	Q3UV88;								
DT	11-OCT-2005,	integrated into UniProtKB/TrEMBL.							
DT	11-OCT-2005,	sequence version 1.							
DT	07-FEB-2006,	entry version 5.							
DE	Adult male bone cDNA, Riken full-length enriched library,								
DE	clone:J98310OH05 product:coll1-like receptor 6, full insert sequence.								

GN Name=tlr6;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Methods Enzymol. 303:19-44(1999).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone; PubMed=16141072; DOI=10.1126/science.1112014;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritch M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilmong L.G., Aldins V., Allen J.E., Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.-P., Choudhary V., Christoflets A., Clutterbuck D.R., Cline M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liu J., Lu J., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakaurchi H., Ng P., Niggli V., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlandi V., Pang K.C., Pavan W.J., Pavoni G., Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schombach C., Sekiguchi K., Sempile C.A., Seno S., Sessa L., Shiba T., Shimada H., Shimada K., Silva D., Sincalir B., Sperling S., Stupka E., Sugizaki K., Sultana R., Takeda Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Matick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuoka S., Kanamori-Katayama M., Suzuki M., Aoki J., Arai K., Iida T., Imanura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome";
 RL Science 309:1559-1563(2005).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone; PubMed=16141073; DOI=10.1126/science.1112009;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RA RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense transcription in the mammalian transcriptome";
 RL Science 309:1564-1566(2005).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone; PubMed=12466851; DOI=10.1038/nature01266;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusica V., Chochia C., Cordani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanei A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltsev L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Perera G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilmong L.G., Wyszewski-Boris A., Yanagisawa M., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Koshikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arai K., Tanaka T., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa J., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone; PubMed=11217851; DOI=10.1038/35055500;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aizawa K., Iwama Y., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Iwama Y., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kanakawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Adono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P., Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmong L., Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S., Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone; PubMed=11042159; DOI=10.1101/gr.145100;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and substructure of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone; PubMed=11076861; DOI=10.1101/gr.152600;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M., Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashtagi K., Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone; PubMed=11076861; DOI=10.1101/gr.152600;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M., Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashtagi K., Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Bone;
 RA Arawaka T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida T., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Niimura N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Takami Y., Waki K., Watabiki A.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (Mar-2004) to the EMBL/GenBank/DBJ databases.
 CC
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 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC
 CC EMBL, AK137502; BAE23384.1; -; mRNA.
 DR MGI; MGI:1341296; T1r6.
 DR GO; GO:0016021; C:integral to membrane; RCA.
 DR GO; GO:0016020; C:membrane; RCA.
 DR GO; GO:0004888; F:transmembrane receptor activity; RCA.
 DR InterPro; IPR004075; IL1_rcpt_1.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_C.
 DR InterPro; IPR003591; LRR_Tyr.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00560; LRR_1; 6.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR01537; INTRINSTRIP.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00368; LRR_TYP; 1.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS0104; TIR; 1.
 KW Receptor.
 SQ SEQUENCE 806 AA, 92394 MW, 6FD0CD4CB8FA5741 CRC64;
 Query Match 75.7%; Score 3144.5; DB 2; Length 806;
 Best Local Similarity 73.9%; Pred. No. 5,5e-188;
 Matches 588; Conservative 97; Mismatches 110; Indels 1; Gaps 1;
 1 MTKDEPIVKSFPVCLMIITVGTRIQFSDGNEPAVDKSKGLIHVPRKLPKTKYLDMS 60
 12 MSQDRKPIVGFPHFCAALIVGSMTPFSNELESNWDSNRMLTHVPKDLPRTRALSIS 71
 61 ONYIAELQVDSWFSFSELTFLRLSHNRILDLVSFKFQDDEYLDLSHNOLOKTSCHPI 120
 72 QNSISELMPSDIFSSELRVLAISHNRISLDPHFPLFQDDEYLDVSNRLONSCCM 131
 121 VSFRLHDSFNDPKALPICKEFGNLSQNLFIQISAMKLOKDLPLPAHLHSYIILDERN 180
 132 ASLRHLDLSFNDPDLVPCVCKEFGNLTJLTFGLISAQKQDLPLPAHLHLSYIILDLVS 191
 181 YIKENEFESLQILNAKTHLVFHPFSLFALIOVNSVNTLGLQTLNTKLANDNCQVPIK 240
 192 YHKGEEESLQIPPTTVLHLVHPNLSFSVQVNSVNAIGHQLQSLNKILDNENCQRLMT 251
 241 FLSELTGSGTLNLTNHIETWKCIVRFQFLMPKPVLYNIYNTIIESIREDFTS 300
 252 FLSELTGSGTLNLTNHIETWKCIVRFQFLMPKPVLYNIYNTIIESIREDFTS 311
 301 KTKLALTIETITNOVFLFSQALATYVFSKXNIMMLTISDTPFIHMLCPHASTFKFLNF 360
 312 ETALSKLMEHVKNQVFLFSKALVSFAKNNIKMLSISDTPFIHWCPCPSSSFFFLNF 371
 361 TONVFTDSFEKCSFLVLETLILQKNGKIDLPKGLMTKMPSLFILDVSNNSLSESGH 420
 372 TONVFTDSFQGCSTLTKRLQTLILQKNGKIDLPKGLMTKMPSLFILDVSNNSLSESHY 431
 421 KENCTWVESIVLITSSNMLTDSVFCPLPRIKVLDLHSNKIKSVYKQVVKLEALQELNV 480
 432 DRTCAWABEIVLVNLSNMLTDSVFCPLPRIKVLDLHSNKIKSVYKQVVKLEALQELNV 491
 481 AENSILTDLPGCSFSSLSVLIIDHNSVSHPSADPFQSCQKMSIKAGDNPFQCTCELRF 540
 492 ASNSILTDLPGCSFSSLSVLIIDHNSVSHPSADPFQSCQKMSIKAGDNPFQCTCELRF 551

QY 541 VKNIQVSEVLEGWPDYSKYCDYPESYRGSPLKDFHMSLSNITLITVIGATMLVLAV 600
 DB 552 VKNIGWVAREVEGPDYSKYCDYPESYRGSPLKDFHMSLSNITLITVIGATMLVLAV 611
 QY 601 TVTSLCYLDLPWYLRWQWOTQTRRAARNIPLEELORNLQFPAFISYSEHSAWYKSL 660
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 ID Q7PPCS MOUSE PRELIMINARY; PRT; 806 AA.
 AC Q7PPCS.
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2003, sequence version 1.
 DT 07-FEB-2006, entry version 14.
 DE Toll-like receptor 6.
 GN Name=TLR6;
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
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 RC STRAIN=C3H/He; TISSUE=Osteoblast;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton W., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfisch A.S., Krzywicki M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences".
 RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C3H/He; TISSUE=Osteoblast;
 RX STRAUSBERG R.;
 DB Submitted (Jul-2003) to the EMBL/GenBank/DBJ databases.
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 CC EMBL, BC055366; AAH53366.1; -; mRNA.
 DR HSSP; Q15399; 1FVY.
 DR SMR; Q7PPCS; 641-796.
 DR Ensembl; ENSMUSG0000051498; Mus musculus.

DR MGI:1341296; TIR6.
 DR GO: GO:0016021; C:integral to membrane; RCA.
 DR GO: GO:0016020; C:membrane; RCA.
 DR GO: GO:0004888; F:transmembrane receptor activity; RCA.
 DR InterPro: IPR004075; IIL_rcpf_1.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_C.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR000157; TIR.
 DR Pfam: PF00560; LRR_1; 6.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF01582; TIR; 1.
 DR PRINTS: PR01537; INTRLNK1RIE.
 DR PRINTS: PR00019; LEURICRPT.
 DR SMART: SM00369; LRR_Typ; 1.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00255; TIR; 1.
 DR PROSITE: PS0104; TIR; 1.
 DR Receptor.
 SQ SEQUENCE 806 AA; 92408 MW; 24830B28EB3C3546 CRC64;

Query Match 75.7%; Score 3143.5; DB 2; Length 806;
 Best Local Similarity 73.7%; Pred. No. 6,4e-188;
 Matches 587; Conservative 98; Mismatches 110; Indels 1; Gaps 1;

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 12 MSQDKRPVIGSFHFVICALALIVGSMTPPNEESAVDVNKRULTHVPKDLPRRTALIS 71
 61 QNYIAELOVSDMSFLSELVTALSHNRIOQLDLVFEKNODELYLDLSHNOLOKISCHI 120
 72 QNSISELMPDISFSELRLVRLSHNRIRSLDFHVELFNQDLEYLDVSHNRLONSISCP 131
 121 VSRHLDSFNDPKALPTICKERGNISQNLFLGISAMKLOKLLPIAHNLSTYIILDLRN 180
 132 ASLRHLDSFNDPDLVPCKEFGNLTKLFLGISAKRFQDLPLPAHNLSTYIILDLRN 191
 131 YYIKENETESIQIILNAKTALHVEHPFSLPAIOVNISVNTGGLQTLNKLNDNCQVFIK 240
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 241 FLSELTRGSLTLNFTLNHIEITWKCLVRFQFLMPKRVYININVTITIESIREDEFTYS 300
 252 FLSELTRGPTLNTVLQHIETWKCSVKLFQFFWPRPVEYININVTITERIDREFTYS 311
 301 KTTLTALTTEHTTNOVFLFSQRLATVSEBNINMILTIDTPIHMLCPHAISTEFTLNF 360
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 372 TONVFTDSVFGCGSTIKRLQTLILLOKNGKLNFKKALMKNNSSLETLVSNNSLSHAY 431
 421 KENCWVESIVVLNLSNNMLTDSVFRCLPPRIKVLIDLHNSNKISKVQVYVKEALQELNV 480
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 612 TGAFPLCIYDLPLMYLTMVCOMTQTRRAHIPLEELQRLNLOPFAFISYSEHDSAWKSEL 671
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 672 LFNLEKDDIRVCIHERNFVPGKSIVENININIEKSYKAIFFVLSPHFIOSEWCHYELEYPAH 731

Qy 721 HNLFEHSGNNIILILEPIPNISIPNKYHKLKALMTORTYIQWKEKSKGLFWANIRAA 780
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RESULT 10

TLR1 HUMAN

ID TLR1 HUMAN STANDARD; PRT; 786 AA.
 AC Q15399; Q15452; Q9UG90;
 DT 31-JAN-2002, integrated into UniProtKB/Swiss-Prot.
 DT 31-JAN-2002, sequence version 2.
 DT 07-MAR-2006, entry version 57.

DE Toll-like receptor 1 precursor (Toll/interleukin-1 receptor-like protein) (TIR) (CD281 antigen).
 GN Name=TLR1; Synonyms=K1AA0012;
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;

NP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Erythrocytemia;
 RX MEDLINE=96118556; PubMed=9435236; DOI=10.1073/pnas.95.2.588;
 RA Rock F.L., Hardman G., Timane J.C., Kastlein R.A., Bazan J.F.;
 RT "A family of human receptors structurally related to Drosophila Toll."
 RL Proc. Natl. Acad. Sci. U.S.A. 95:588-593(1998).
 RN [2]

NP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Bone marrow;
 RX MEDLINE=96051387; PubMed=7584026; DOI=10.1093/dnares/1.1.27;
 RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
 RA Sato S., Nagase T., Seki N., Ishikawa K., Tabata S.;
 RT "Prediction of the coding sequences of unidentified human genes. I.
 RT The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by
 RT analysis of randomly sampled cDNA clones from human immature myeloid
 RT cell line KG-1."
 RL DNA Res. 1:27-35(1994).
 RN [3]

NP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Brain;
 RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
 RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glasel S.,
 RA Ansoerg W., Boecker M., Bloecker H., Bauersachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
 RA Mewes H.-W., Oltenswelder B., Obermaier B., Tampe J., Heubner D.,
 RA Wambutt R., Korn B., Klein M., Poustka A.;
 RT "Towards a catalog of human genes and proteins: sequencing and
 RT analysis of 500 novel complete protein coding human cDNAs."
 RL Genome Res. 11:422-435(2001).
 RN [4]

NP PROTEIN SEQUENCE OF 25-39.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.U.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites."
 RL Protein Sci. 13:2819-2824(2004).
 RN [5]

RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF TIR DOMAIN.
 RX MEDLINE=20531768; PubMed=11081518; DOI=10.1038/35040600;
 RA Xu Y., Tao X., Shen B., Horng T., Medzhitov R., Manley J.L., Tong L.;
 RT "Structural basis for signal transduction by the Toll/interleukin-1
 RT receptor domains."
 RL Nature 408:111-115(2000).

CC -!- FUNCTION: Participates in the innate immune response to microbial
 CC agents. Cooperates with TLR2 and modulates the response to
 CC microbial constituents. Acts via MyD88 and TRAF6, leading to NF-
 CC kappa-B activation, cytokine secretion and the inflammatory

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CC response (By similarity).
CC -1 SUBUNIT: Binds TLR2 via their respective extracellular domains.
CC Binds MyD88 via their respective TIR domains (By similarity).
CC -1 SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
CC phagosomes (By similarity).
CC -1 TISSUE SPECIFICITY: Ubiquitous. Highly expressed in spleen, ovary,
CC peripheral blood leukocytes, thymus and small intestine.
CC -1 SIMILARITY: Belongs to the Toll-like receptor family.
CC -1 SIMILARITY: Contains 8 LRR (leucine-rich) repeats.
CC -1 SIMILARITY: Contains 1 TIR domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs license
CC -----
DR EMBL, U86540; AAC34137.1; -; mRNA.
DR EMBL, D13637; BAA02801.2; ALT_INIT; mRNA.
DR EMBL, AL050262; CAB43364.1; -; mRNA.
DR PIR, T08664; T08664.
DR PDB, 1FVY; X-ray; A=625-785.
DR Ensembl, ENSG00000174125; Homo sapiens.
DR H-InvDB, HIT0004160; -.
DR HGNC, HGNC:11847; TLR1.
DR MIM, 601194; gene.
DR GO, GO:0005887; C:integral to plasma membrane; TAS.
DR GO, GO:0045335; C:phagocytic vesicle; ISS.
DR GO, GO:0005886; C:plasma membrane; TAS.
DR GO, GO:0004888; C:transmembrane receptor activity; NAS.
DR GO, GO:0042497; C:transmembrane lipoprotein binding; ISS.
DR GO, GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR GO, GO:0042495; P:detection of triacylated bacterial lipoprotein; ISS.
DR GO, GO:0006955; P:immune response; TAS.
DR GO, GO:0042116; P:macrophage activation; NAS.
DR GO, GO:0045410; P:positive regulation of interleukin-6 biosyn. .; ISS.
DR GO, GO:0042535; P:positive regulation of tumor necrosis facto. .; ISS.
DR GO, GO:0007165; P:signal transduction; TAS.
DR InterPro, IPR004075; IL1 rcpt_1.
DR InterPro, IPR001611; LRR.
DR InterPro, IPR000483; LRR_C.
DR InterPro, IPR003591; LRR_C_Typ.
DR InterPro, IPR000157; TIR.
DR Pfam, PF00560; LRR_1; 7.
DR Pfam, PF01463; LRRCT; 1.
DR Pfam, PF01582; TIR; 1.
DR PRINTS, PR01537; INTRLNKTRIP.
DR PRINTS, PR00019; LEURICHRPT.
DR SMART, SM00082; LRRCT; 1.
DR SMART, SM00255; TIR; 1.
DR PROSITE, PSS0104; TIR; 1.
KW 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immune response; Inflammatory response; Innate immunity;
KW Leucine-rich repeat; Membrane; Polymorphism; Receptor; Signal;
KW Transmembrane.
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DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Toll-like receptor 1.
GN Name=TLR1;
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OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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OC Homo.
OX NCBI_TaxID=9606;
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RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
CC Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
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CC EMBL, BC109094; AA109095.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
KW Receptor.
SQ SEQUENCE 786 AA; 90290 MW; 1406C6FB5847F58 CRC64;

Query Match 68.1%; Score 2830; DB 2; Length 786;
Best Local Similarity 69.5%; Pred. No. 2,5e-168;
Matches 540; Conservative 92; Mismatches 143; Indels 2; Gaps 1;

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Db 725 STILILBPIPNQSIIPNTHKYLKALMTQRTYIQMPKESKRGLPFANIRAAFNMKLT 781

RESULT 12
Q32MK4_HUMAN PRELIMINARY; PRT; 786 AA.
AC Q32MK4;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Toll-like receptor 1.
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GN Name=TLRL;
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
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 RC TISSUE=PCR resequenced clones;
 RX MEDLINE=22388257, PubMed=12477932, DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR resequenced clones;
 RG NIH MGC Project;
 RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
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 DR EMBL, BC109093; AAI09094.1; -; mRNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 KW Receptor.
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 Query Match 68.1%; Score 2829; DB 2; Length 786;
 Best Local Similarity 69.5%; Pred. No. 2,9e-168;
 Matches 540; Conservative 91; Mismatches 144; Indels 2; Gaps 1;
 QY 12 FHFVCLMIITVGTTRIOFSDGNFPAVDKSRGLIHPKDLPLTKVLDMSONTIAELQVSD 71
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 QY 192 QILNAKTLHVPHPSPALPQNIIVNTLIGCQLQNLTK-LVDDNCQVPIKFLSELTRGS 249
 DB 185 QDFNESHAIIVPTNKEFHFILDVASKVIVANLELSIKVLDNKSYSFLSLIAKLQTNP 244
 QY 250 TLNLTNLNHIETTKCLVRFQPLWPKPYEYINIVLTIIIESIRBEDFTYSKTTIKALTI 309
 DB 245 KLSNLTNIIETTMSFIRILQLVHHTVWPSISVVKLQGLDPRDPYSGTSLKALSI 304
 QY 310 EHTIQVPLFSQALATYVSENNIMLTISDTPFIHMLCPHAPSTFKFLNFTQNFPTDSI 369
 DB 305 HQVADVDFGPOSYIYEIIFSNMNIKQFTVSGTRVMHMLCPSTXISPLHLDFSNMLTDTIV 364

QY 370 FEKSTVLVLETLILQKNGKLDLKVGLMTKMPSLIEDVSMNSLESGRHKENCTWVS 429
 DB 365 FENCGHLETLLETLILQMNQKLSKIAEHTTQMKSLQQLDISGNSVYBEKKGDCSWTS 424
 QY 430 IVNLISNMILDSVFRCLPPRIKVIDLHSNKIKSVPKQVVKLEALQELNVAFNSITDLP 489
 DB 425 LLSLNMSSNILLDTIFRCPLPPIKVIDLHSNKIKSIPKQVVKLEALQELNVAFNSITDLP 484
 QY 490 GCGSPSSISVLIIIDHNSVSPADPFQSCQKRSIYAGNPPQCTELDEFVKNIDQVS 549
 DB 485 GCGSPSSISVLIIIDHNSVSPADPFQSCQKRSIYAGNPPQCTELDEFVKNIDQVS 544
 QY 550 EYLEGWPDYKCDYDESYGSLPKDFHNSLSNLTLLIVTIGATVLAIVTSLCIYL 609
 DB 545 EYLEGWPDYKCDYDESYGSLPKDFHNSLSNLTLLIVTIGATVLAIVTSLCIYL 604
 QY 610 DLPWYLRVQWQTRRRARNIPLELOQNLQFHAFTSYSHDSAMVSKELVYLEKEDI 669
 DB 605 DLPWYLRVQWQTRRRARNIPLELOQNLQFHAFTSYSHDSAMVSKELVYLEKEDI 664
 QY 670 QICLHERNVPKSIIVENTINICEKSYKSIIFVLSRPFVQSEWCHVELYFAHNLPHESGN 729
 DB 665 QICLHERNVPKSIIVENTINICEKSYKSIIFVLSRPFVQSEWCHVELYFAHNLPHESGN 724
 QY 730 NLILILEPIPNOSIPNKYHKLKALMTORTYLOMPKESKRGLEFMANIPAEFMKLT 786
 DB 725 SLILILEPIPNOSIPNKYHKLKALMTORTYLOMPKESKRGLEFMANIPAEFMKLT 781
 RESULT 13
 ID 05FMG5_HUMAN PRELIMINARY; PRT; 786 AA.
 AC 05FMG5;
 DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Toll-like receptor 1.
 GN Name=TLRL;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;
 RX MEDLINE=22388257, PubMed=12477932, DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;
 RA Director MGC Project;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

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 CC -----
 DR EMBL: BC089403; AA89403.1; -; mRNA.
 DR SMR: OSFMC5; 625-785
 DR Ensembl: ENSG00000174125; Homo sapiens.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro: IPR004075; IL1 rcpt 1.
 DR InterPro: IPR003016; LipoYL_BS.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_C.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR001574; TIR.
 DR Pfam: PF00560; LRR_1; 7.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF01582; TIR; 1.
 DR PRINTS: PRO1537; INTRLNRLP.
 DR PRINTS: PR00019; LEURICRPT.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00255; TIR; 1.
 DR PROSITE: PS00189; LIPOYL; UNKNOWN_1.
 DR PROSITE: PS0104; TIR; 1.
 DR RECEPTOR.
 DR SEQUENCE 786 AA; 90267 MW; 6B9B673F6E47BF3A CRC64;
 SQ
 Query Match 68.1%; Score 2828; DB 2; Length 786;
 Best Local Similarity 69.5%; Pred. No. 3.3e-168;
 Matches 540; Conservative 92; Mismatches 143; Indels 2; Gaps 1;
 QY 12 FHFVCLMIITVTRIQFSDGNEFPAVDKSRGLIHVPKDIPLTKYVLDMSQNTYIAEQVSD 71
 DB 5 FHFALIFMLIDQIRIQLSSESEFLVDRSKGLIHVPKDSQKTTILNISQNTYISELMTSD 64
 QY 72 MSFSELTVLRISHNRIOQLDLSVFKENDLEYLDLSHNOLOKISCHPVRSHRLDLSFN 131
 DB 65 ILSLKLRLIISHNRIOQLDLSVFKENDELEYLDLSHNLKVKISCHPVRNLKHLDSLGN 124
 QY 132 DFKALPICKERGNLSQNLFLGLSANKLOQLDLPLAHLHLSYLLDLRNYIYIKENETSL 191
 DB 125 AFDALPICKERGNMSQNLFLGLSTHLEKSSVLPFAHLNISKVLVLGELYGEKEDPGQL 184
 QY 192 QILNAKTHLVHPPLSLPAIQVNISVNTLGGCQLTNIK--LNDNCQVFIKRLSELTRGS 249
 DB 185 QDFNTESLHIVPTNKEFHFIIDVSKVTANLELSNIKCVLEDNKCSYFLSLAKLQTNP 244
 QY 250 TLNFTLNIHETWTKLVVPOFLMKPVEYLNIVNLTIIESREDFYSKTTLKALNI 309
 DB 245 KLSLTLNNIETWMSFIRILQVHTTWYFISISVNLQGGQUDPRDFYSGTSLKALSI 304
 QY 310 EHIITQVFLFSOTALYTVFSENNIMMLTISDTPFIHMLCPHASPTEKPLNFTQNVFTDSI 369
 DB 305 HQVAVDVGFPQSYIYEIIFSNMNIKNFTVSGTRMVMMLPSKISPLNLDNFNNLLTDIV 364
 QY 370 FEKSGTLYKLEFLTIQKNGKLDLFXVGLMTKMPSEIETIDVWNSISGRHKENCTWBS 429
 DB 365 FENCHLTELLEFLTIQMNQKELSKIAEWTTQMKSIQOQDIDISONSYSYDEKGDGCSWTKS 424
 QY 430 IYVNLSSNMLTDSVFRCLPRRIKYLDLHSNKIKSPKQVNVLEALQELNVAFNSLTDLR 489
 DB 425 LLSLWSSNITLDTDTIFRCLPPRIKYVLDHSNKIKSPKQVNVLEALQELNVAFNSLTDLR 484
 QY 490 GCGSSSSSLVLIIDHNSVSHPADFPQSCQKRSIKAGDNPFQCTCELEFVKNIDQVS 549
 DB 485 GCGSSSSSLVLIIDHNSVSHPADFPQSCQKRSIKAGDNPFQCTCELEFVKNIDQVS 544
 QY 550 EYLBGMPDSYKCDYPSYRSGPLKDFHMSLSNCITLLIVTIGATMLVLAIVTSTCIYL 609
 DB 545 EYLBGMPDSYKCDYPSYRSGPLKDFHMSLSNCITLLIVTIGATMLVLAIVTSTCIYL 604
 QY 610 DLPLWLRVCOMTQTRRRARNIPLBELQNLQPHAFISYSEHSDAMVYSLEYLVEKEHI 669
 DB 605 DLPLWLRVCOMTQTRRRARNIPLBELQNLQPHAFISYSEHSDAMVYSLEYLVEKEHI 664

QY 670 QICLHERNFVPEKSIIVENINCIEKSYKSIIVLSPNVQSEWCHYEYFAHNLFEHGSN 729
 DB 665 QICLHERNFVPEKSIIVENINCIEKSYKSIIVLSPNVQSEWCHYEYFAHNLFEHGSN 724
 QY 730 NILILLEPRIPONGSPNKYHKLKAMTORTYQWPEKSKGLFANIRAAFNMLT 786
 DB 725 SLILLEPRIPQSYSPSSYHKLKLSIMARRTYLEWPEKSKGLFANIRAAFNMLT 781
 RESULT 14
 ID Q6F164_HUMAN PRELIMINARY; PRT; 786 AA.
 AC Q6F164;
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE TLR1 protein.
 GN Name=TLR1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo
 NCBI_Taxid=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: CR533562; CAC38593.1; -; mRNA.
 DR SMR: OSF164; 625-785.
 DR Ensembl: ENSG00000174125; Homo sapiens.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro: IPR004075; IL1 rcpt 1.
 DR InterPro: IPR003016; LipoYL_BS.
 DR InterPro: IPR000483; LRR_C.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR001574; TIR.
 DR Pfam: PF00560; LRR_1; 7.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF01582; TIR; 1.
 DR PRINTS: PRO1537; INTRLNRLP.
 DR PRINTS: PR00019; LEURICRPT.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00255; TIR; 1.
 DR PROSITE: PS00189; LIPOYL; UNKNOWN_1.
 DR PROSITE: PS0104; TIR; 1.
 DR SEQUENCE 786 AA; 90163 MW; DB6B54E684009284 CRC64;
 SQ
 Query Match 67.8%; Score 2817; DB 2; Length 786;
 Best Local Similarity 69.2%; Pred. No. 1.6e-167;
 Matches 538; Conservative 92; Mismatches 145; Indels 2; Gaps 1;
 QY 12 FHFVCLMIITVTRIQFSDGNEFPAVDKSRGLIHVPKDIPLTKYVLDMSQNTYIAEQVSD 71
 DB 5 FHFALIFMLIDQIRIQLSSESEFLVDRSKGLIHVPKDSQKTTILNISQNTYISELMTSD 64
 QY 72 MSFSELTVLRISHNRIOQLDLSVFKENDELEYLDLSHNLKVKISCHPVRNLKHLDSLGN 131
 DB 65 ILSLKLRLIISHNRIOQLDLSVFKENDELEYLDLSHNLKVKISCHPVRNLKHLDSLGN 124
 QY 132 DFKALPICKERGNLSQNLFLGLSANKLOQLDLPLAHLHLSYLLDLRNYIYIKENETSL 191
 DB 125 AFDALPICKERGNMSQNLFLGLSTHLEKSSVLPFAHLNISKVLVLGELYGEKEDPGQL 184
 QY 192 QILNAKTHLVHPPLSLPAIQVNISVNTLGGCQLTNIK--LNDNCQVFIKRLSELTRGS 249
 DB 185 QDFNTESLHIVPTNKEFHFIIDVSKVTANLELSNIKCVLEDNKCSYFLSLAKLQTNP 244

Job time : 162 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 2, 2006, 22:53:30 ; Search time 22 Seconds
(without alignments)
3461.297 Million cell updates/sec

Title: US-10-732-796A-12

Perfect score: 4154

Sequence: 1 MTGXKEPIVKSFPVFCVLMIL.....IPAAFNKTLVTENNDVKS 796

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: pir80:*
2: pir1:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2820	67.9	786	2	T08664 Toll protein-like
2	406.5	9.8	1097	2	A29943 Toll protein precu
3	285.5	6.9	1066	2	T15864 hypothetical prote
4	274	6.6	1385	2	T13887 c1r protein - fru1
5	268.5	6.5	1039	2	T22117 hypothetical prote
6	268.5	6.5	1389	2	T13852 gene wheeler prote
7	244.5	5.9	987	2	T50850 receptor protein K
8	238	5.7	662	2	S42799 gaip precursor - h
9	235	5.7	1531	2	T42218 slit-1 protein hom
10	233	5.6	1469	2	B3665 slit protein 2 pre
11	233	5.6	1480	2	A3665 slit protein 1 pre
12	230.5	5.5	921	2	B86234 hypothetical prote
13	226.5	5.5	559	2	T42998 Ras-binding protei
14	225.5	5.4	1025	1	A57676 protein kinase Xa2
15	225	5.4	855	2	T07015 Cf-4A protein - to
16	223	5.4	1091	2	A58532 glial cell membran
17	221	5.3	1143	2	T10636 hypothetical prote
18	221	5.3	1692	2	A33988 adenylate cyclase
19	219	5.3	560	2	A60164 platelet membrane
20	217	5.2	907	2	JG0193 G protein-coupled
21	216	5.2	572	2	T30947 hypothetical prote
22	214.5	5.2	1134	2	T04587 hypothetical prote
23	212	5.1	853	2	T17461 glial cell membrane
24	211	5.1	661	2	T56258 RPIOS - mouse
25	210	5.1	890	2	E84846 probable receptor-
26	210	5.1	2026	1	OYBYR adenylate cyclase
27	208.5	5.0	983	2	G84524 probable disease r
28	207	5.0	800	2	H84740 hypothetical prote
29	207	5.0	1839	1	OYBYK adenylate cyclase

30	206	5.0	855	2	T17460 disease resistance
31	205	4.9	1013	2	T10659 probable serine/ch
32	205	4.9	1778	2	AF1116 intermin protein
33	204.5	4.9	1523	2	T13953 MEGR5 protein - ra
34	204	4.9	613	2	A88684 protein ACT.2 (imp
35	204	4.9	679	2	T20713 hypothetical prote
36	204	4.9	907	2	JE0176 orphan G protein-c
37	203.5	4.9	845	2	T07039 Hcr9-0 protein - t
38	203	4.9	707	2	T28418 ORF MSY257 leucine
39	202.5	4.9	611	2	T28171 hypothetical prote
40	202	4.9	1166	2	F96598 protein F20N2.4 il
41	200	4.8	1232	2	T05322 hypothetical prote
42	198.5	4.8	910	2	G84648 probable disease r
43	196	4.7	980	2	H84632 probable receptor-
44	195	4.7	910	2	B96770 hypothetical prote
45	195	4.7	1134	1	A29944 chaoptin precursor

ALIGNMENTS

RESULT 1

T08664

Toll protein-like receptor DKFP54710610.1 - human

QY 490 GCGSSSSLSVLLIDHNSVSPADPFQSCQKRSIKAGDNPQCTCELRFPYKNIDQVSS 549
DB 485 GGGSSSSLSVLLIDHNSVSPADPFQSCQKRSIKAGDNPQCTCELRFPYKNIDQVSS 544
QY 550 EYLEGMPSYKCDYFESYSGSPKDPHMSLSCNTLLVTIGATMVLVAVTSLCTYL 609
DB 545 EYLEGMPSYKCDYFESYSGSPKDPHMSLSCNTLLVTIGATMVLVAVTSLCTYL 604
QY 610 DLPWYLRMVCQWOTRRRRARNIPLEELQRLQPHAFISYSEHDSAMVKESELYLEKEDI 669
DB 605 DLPWYLRMVCQWOTRRRRARNIPLEELQRLQPHAFISYSEHDSAMVKESELYLEKEDI 664
QY 670 QICLHERNFVPGKSIYENIINCIEKSYKSIYVLSFNPVQSEWCHELYEFAHNLPHESGN 729
DB 665 QICLHERNFVPGKSIYENIINCIEKSYKSIYVLSFNPVQSEWCHELYEFAHNLPHESGN 724
QY 730 NLLILLEPIPNQSIYENIINCIEKSYKSIYVLSFNPVQSEWCHELYEFAHNLPHESGN 786
DB 725 SLILILEPIPNQSIYENIINCIEKSYKSIYVLSFNPVQSEWCHELYEFAHNLPHESGN 781

RESULT 2

A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C/Accession: A29943
R/Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A/Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, as
A/Reference number: A29943; MUID:88135760; PMID:2449285
A/Accession: A29943
A/Molecule type: DNA
A/Residues: 1-1097 <HMS>
A/Residues-references: UNIPROT:P08953; UNIPARC:UPI0000124883; GB:M19969; GB:J02682; NID:915
C/Genetics:
A/Gene: FlyBase:Fl
A/Cross-references: FlyBase:FBgn0003717
C/Keywords: transmembrane protein
F.1-17/Domain: signal sequence #status predicted <STG>
F.18-1097/Product: Toll protein #status predicted <MAT>

Query Match 9.8%; Score 406.5; DB 2; Length 1097;
Best Local Similarity 22.5%; Pred. No. 1.5e-18;
Matches 203; Conservative 145; Mismatches 321; Indels 235; Gaps 38;

QY 41 RGLIHPKD-----LPLKTKVLDNSQYIAELQVSDMSFLSELTVLRISNRQL 90
DB 160 RRLTHIPANLLTDMENLSHLEIRANIEEMPSHLFDLE-----NLESIEFGSKLRQ 211
QY 91 LDLSYFKFNQDLEVLDSHNOLOKISCH-----PIVSFRHL--- 126
DB 212 MERGIFGKMPKYLKQNLMSNQLNHTKDPBGATSVLGTDIDNGIEBQPHDVFALHTNV 271
QY 127 ---DLSFNDFKALP-----ICKEFGNLSQLNFIQLSAMKL 158
DB 272 TDINISANLFRSLPQGLFDHNGHNEVRMLNNRVPPLATPSLFLANQPELQLRLRA-EL 330
QY 159 QKL---DL-----PIAHLHSYLLDLRNYIKENETE---SLQTLAKTIAHVFHPSLFA 210
DB 331 QSLPDLDFEHSQTQINISLGDNLTKTLPTATLLEHQVNLISLPLSNRLTHL---PDSLFA 387
QY 211 IQVNI-----SVNTLGCQLQTNIKLNDNCOVFIKFLSELTRGSTL 251
DB 388 HTTNLTDLRLDENLTLGSGDIFSNIGNLVTLVMSKNRLRTIDSRAFVS-----TWGLRH 442
QY 252 LNFNLNHLIETTKCLVRFQFLMPKREVE-----LNIYNLTII-----ESIREE 295
DB 443 LHLHDNDIDLQOPLDIDIMQTOINSPFGYMGHGLTLNLNNSGIIIFYVNDKATMQLRL 502
QY 236 DFTYSKTLIKALTIIHTINQVFLFSGOTALYTVFS-----ENKIMML 336

DB 503 DLSTN-NISSLCYDILA-----FLSQRLHVNMTNINKRLRALPEDVHLCSTYNNNLVHV 556
QY 337 TISDTPFIMLCPHAPSTFKFLNFTQNY-----FTDSIFEKSTVYKLETLILQKNGLDL 392
DB 557 DLNDNP---LVCD---CTLWFIQLVGRVGHKQYSQFRLDRVLVCSQPNVLEGPVQI 611
QY 393 FVVGIMTQDMSLEILLVDSWNSLESGRHKE---NC---TWVESIVVLNLSNMULTSV 444
DB 612 EPQTLICP-----LDPS-----DDPRERKCPGRCNCCHVRTYDKALVINCISGNLTVHR 660
QY 445 FRCLPERRIKVLDLH--SNKIKSVK-qVVKLEALQELVAFNSLTDLGGCSFSSLSVLI 501
DB 661 LPLHKNQQLMELHENVNLTLLRLPSANTPGYBSVSLHLAGNNLTSTVDQLPTLTHLD 720
QY 502 IDHNSVSPSA---DFQSCQKRSIKAGDNPQCTCELRFEV---KNIDQVSEVLEG 554
DB 721 ISMNLQMLNATVGLFRLRTMKRVRKVSQGNPWDCCTAKPLLLFTQNPFI-----G 774
QY 555 WPDYKCDYPESYSGSPKDPHMSLSCN-----ITLLVTIGATMVLVAVT--- 602
DB 775 DRENEMCVNAE---MPTR---MVSLSTNDICPAKGVFIALAVIALTGLLAGFTALY 827
QY 603 ---TSLGITYLDLPWYLRMVCQWOTRRRRARNIPLEELQRLQPHAFISYSEHDSAMVKS 658
DB 828 YKQTEIKIWL---YAHNLWVTE-----EDLDKQKGFATSYSHKQSFLED 875
QY 659 ELVPYLE--KEDIQICLHERNFVPGKSIYENIINCIEKSYKSIYVLSFNPVQSEWCHELY 716
DB 876 YIVPQLEHGPQKFOUCYHERDMVCGHNPENIMRSVADSRRITIIYLSQNFISKSEARLEF 935
QY 717 YFAHNLPHESGNLILILEPIPNQSIYENIINCIEKSYKSIYVLSFNPVQSEWCHELY 776
DB 936 RAHRSALNEGSRRIIIVYSDI--GDVEKLEDEIKAVLKMTYIKWQDP-----WFWDK 988
QY 777 IRRA 780
DB 989 LRFA 992

RESULT 3

T15864
Hypothetical protein C56E6.6 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15864
R/Fulton, L.
submitted to the EMBL Data Library, November 1995
A/Description: The sequence of C. elegans cosmid C56E6.
A/Reference number: S69019
A/Accession: T15864
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1066 <FULL>
A/Cross-references: UNIPROT:Q18902; UNIPARC:UPI00000811D7; EMBL:U39996; NID:g1055114; PI
C/Genetics:
A/Gene: CESP:C56E6.6
A/Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 833/3; 892/3; 9

Query Match 6.9%; Score 285.5; DB 2; Length 1066;
Best Local Similarity 21.0%; Pred. No. 1.1e-10;
Matches 140; Conservative 123; Mismatches 220; Indels 185; Gaps 30;

QY 21 IVGTRIQFSDGNEFAVDKSRGLIHPKDLPLKTKVLDMSQNYIAELQVSDMSFLSELTV 80
DB 421 LAGNQLDITENMGSSSSS-----ELKSLNLAHKKHISRSRPSDLDNLO 468
QY 81 LRLSHNRQLDLSYFKFNQDLEVLDSHNOLOKISCH-----PIVSFRHLD----- 127
DB 469 LRLSHNRITITSMFTSRLMLRYDLDSHNRILIKILPSALYQLPALDVLHLDHNNLNEID 528
QY 128 ---LSFNDFKALPI-----CKEFGNLSQLNFIQLSAMKQKLDLPIAHLHLSYI 174
DB 529 RDAFRSFDLSLKLKSHNAFRFRSCFGLSGISQVHQLDLSNQINEIDIFCIAR----- 582

QY 175 LDDLENNYIKENETSLOIIMAKTHLVHPHPSLAIQVN---ISVTV---LGLQLTN 227
Db 563 --GIKKLSLANSVKE--INRKLQ---DATELTSIDISHNGIIDVSDAFCECRKLSH 634
QY 228 IKLND-----NCQVFIKPLSELTRGSTLLNFTLNHIETWCKLAVFOPLMCKPVEY 280
Db 635 IKLSNNYIRNLWKGRVCIPIWISHLT---TFCFTEKHEHERTIS----FSYIIVDSQL 686
QY 281 LNIYVLT-----TESIREEDF-----TYSKTKLALTEHITNOV 316
Db 687 TSFGNLSTLSFANNKVDSDIEDGAFENLTLKILDLNNPVMSWSPAFRDLs--HSISSI 744
QY 317 FLFSGTALYTV--FSENNIMMLTISDT----- 341
Db 745 NM-ANTGTFSPMKFHSRHSIQSLNISCNKIYELSEKDLAPLTKVALDISHNNLKOISSMA 803
QY 342 --PFIHMLCPHAPSTFEKFLNFTQNVFTDSIFEKSCSTLYLETLILQKNGKLDL--FKVG 396
Db 804 FEPRLHL-----KQLNVSANPIYTHLMEHIQOLYKL-----YNIDMARPYDIS 847
QY 397 LMTKDMPELEIL--DVSNNSLDESGHKNCTWVESIVVLNLSNNMLDSVRCPLP-RIK 453
Db 848 SILSNLPLRIHTIYVDIKESALDRPFYADTRLRLHLVAGNRLTKIEVGAPATIRGFSVR 907
QY 454 VLDDSNKIKSVKQVNVLELALQELNVAFNSLTD--LPQGSF--SSLSLVLLIDHNSVHP 510
Db 908 I-EINSSIEEPSPSI--FDLITGISLSTSLTDKTLTPPNPOSTVAPAVNOGHTILH- 963
QY 511 SADPFQSCQMKRSIRAGNPFQCTELR---EFVNKIDOVSEVLEGPDSYKCDYPESTY 567
Db 964 -----SLETKNNPIKCDQCFKMDDFIRVTFSLSDHSHSDPDKVECADAGS- 1010
QY 568 RGSPLKDF 575
Db 1011 --SNLESF 1016

RESULT 4
T13887
clr protein - fruit fly (Drosophila melanogaster)
i:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13887
R:Chang, C.; Beachy, P.A.
Mech. Dev. 47, 225-239, 1994
A:Title: Expression of a novel Toll-like gene spans the parasegment boundary and contri-
butes to the formation of the posterior parasegment in Drosophila
A:Reference number: Z17805; MUID:95151581; PMID:7848870
A:Accession: T13887
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1385 <CH1>
C:Cross-references: UNIPROT:Q24591; UNIPARC:UPI000016C024; EMBL:S76155; NID:g913247; PIR
C:Genetics:
A:Cross-references: FlyBase:FBgn0004364
A:Note: clr

	Query Match	6.6%; Score 274; DB 2; Length 1385;
	Beet Local Similarity	21.6%; Pred. No. 9.1e-10;
	Matches	206; Conservative 160; Mismatches 311; Indels 278; Gaps 52;
Oy	41 RGLHPVDPDLKTKVLDMSONYTAELQVSMF--LSELTVLTLSHNRIGLDLSVPKF	98
	: :: :: :: :: :: :: :: :: :	:
Dd	300 KGLHRLLEQL---LVLDLSGNQLTDHHVDNSTFAGLRIRLVNLSSNALRRISKTKE	355
Oy	99 NQDELYLDLSHNLOKI---SCHPIVSFRHLDSFND-----FKALPI-----	138
	:::: :: :: :: :: :: :: :: :: :	:
Dd	356 LYLFIQIDLMRNNSIGHIEGAFLPLYNLHTLNLAENRRLHTDNNRIPNGLVYLTKLTINN	415
Oy	139 -----CSEFGNLSQNFLLGSAMKLQKLDLPLAHLHSYT-IIDLRYNYIKENETESL	191
	:::: :: :: :: :: :: :: :: :: :	:
Dd	416 LVSIYESAFNCSCSLKELDLSNQDT---VPEAAQDLSMLKTLDGENDISEFKNTTE	472

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QY 192 QILNAKT-LHI-VFH-----PTS-LPAQWNISVNTLGCQLINIKLN--DDMCQYFI----- 239
Db 473 RNLMQGLGLRLIDRKIGNITVGMFODLPRLSVLNIAKNRIGSIEGAFDKTTELEAIRLD 532
QY 240 -KPLSEL-----TRGSTP-LNFTLNHIETTKCLVRVFOFLW-PRKVEYUINYNLTIES 291
Db 533 KKFPLTDINGITPATIASLIMLNSBNHL--VN-----FDYAFIBSNLKMIDHG-NYIEA 583
QY 292 -----IREE-----DFTYSK-TTLKALTEIHTNOVL-----FS 320
Db 584 LGNYVKLOEERIVTTLTDASHNRITIEIGAMSVPSNIIEFFINNIIIGQIQANTFVDKTRLA 643
QY 321 QITALY-TYFSEMNIMLTIS-----DTP----- 343
Db 644 RVDDYAVANTLSKISINALRVAIPVSAEKVPYBEFYLGNPPECCSMEWLORINNLITROPH 703
QY 344 -----IHMLCPHA-----PSTPKFLNFPQ----- 362
Db 704 VVDIGNIECLMPHRSAPLRPLASISADFPYCKIESHCPRCHCEBYEQCEBYICPENC 763
QY 363 NVFTDSIFE-----KC-STLVKLETLILQKNGLNDLFKVGIMTRDMSELTIDVSNLSLE 416
Db 764 SCFHDATATNITVDCGRDIALALPNRIPO--DVSDLYLDG--NNMPELEVGH----- 812
QY 417 SGHKEKNCWTVESTIVLNLSSNMTLDSYFRLCPRIKYLDSHKNITSVP-KOYVKEAL 475
Db 813 TGRNRRLALYLNANIMLTLQNGSLAOLV-----NLRLIENNNKLTALBEGTERRSGLLL 866
QY 476 QELNVAFNSLIDLDCGCSFS---SLSVLIIDHNSVSHSADFPSCQCMRSIKXAGDNFPQ 532
Db 867 RELVYHNMLTHISN-ATFEPVLSLEVLRLNNRKS--SLPHLOYRHSLOGLTLGRNAMS 923
QY 533 CTC-----ELREFVKNIDOVSSSEVLGMPDSYKCY-----PESYRGSPLK 573
Db 924 CRCQQLBELAQFVSD---NAMVVURDAHDYICLDAGIKREBELIGNLANGPDC---SDLL 976
QY 574 DFHNSSELSCN-----ITLLIVTIGATMLVLAVTVTSLCTIYLDLPTWLRWCQ 620
Db 977 DASASNISSSODLAGGYRLPLLAVALVLIIFLDVLLIIVFPRSEVRMLFAHYGR-VCE 1035
QY 621 WTQRRRRARNTPLBELQNLQFHAFISYSEHDSAMVSELVPYE--KEDIQICLHERNF 678
Db 1036 -----PRFEDAGKL-YDAIILHSEQDYFCVCRNIAALEHGRPPRLCTIOQDL 1083
QY 679 VPKGSIVENIINCIEKSYKIFVLSPNFVOSGCHYEYLFAPHNMLFHEGSNNLT--LTL 736
Db 1084 PRQASHQ-LVEGARASRKILLVLTIRMLATENMRIEF---RAAFHESLRGLAGKQVLII 1138
QY 737 EPIRQNSIPNKYIKLALMTQRYLQWPKESKGL-----FANITRAAFNMKT 786
Db 1139 E---ETSVSAEADVAEL---SPYIK--SVPSNNLTCDRYFMFKLTVYALPIEIS 1185

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RESULT 5
T22117
hypocholesterol protein F43C1.1 - *Caenorhabditis elegans*
Cj:Species: *Caenorhabditis elegans*
Cj:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cj:Accession: T22117
Rj:Jasael, B.; Smith, A.
submitted to the EMBL Data Library, December 1994
Aj:Reference number: Z19519
Aj:Accession: T22117
Aj:Status: Preliminary; translated from GB/EMBL/DBDj
Aj:Molecule type: DNA
Aj:Residues: 1-1039 <MIL>
Aj:Cross-references: UNIPROT:Q99564; UNIPARC:UPI000013BF7A; EMBL:Z46537; PIDD:CAA87056.1
Aj:Experimental source: clone F43C1
Cj:Genetics:
Aj:Gene: CESP:F43C1.1
Aj:Map position: 3
Aj:Introns: 83/1; 105/1; 185/3; 283/3; 358/3; 386/1; 438/2; 490/2; 516/3; 609/3; 686/2; 7

receptor protein kinase homolog [imported] - soybean

C:Species: Glycine max (soybean)
C:Date: 21-Jul-2000 #sequence__revision 21-Jul-2000 #text_change 31-Dec-2004
C:Accession: T50850

R:Yamamoto, E.; Karakaya, H.C.; Knapp, H.T.
Biochim. Biophys. Acta 1491, 333-340, 2000

A:Title: Molecular characterization of two soybean homologs of Arabidopsis thaliana CLAV

A:Reference number: 225262

A:Accession: T50850

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-987 <YAM>

A:Cross-references: UNIPROT:Q9W6A7, UNIPARC:UPI00000AC3C7, EMBL:AF197947, PIDN:AAF59906.

A:Gene: CLV1B

C:Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat ho

Query Match 5.9%; Score 244.5; DB 2; Length 987;
Best Local Similarity 19.5%; Pred. No. 4.9e-08;
Matches 177; Conservative 121; Mismatches 224; Indels 387; Gaps 42;

Qy 45 HVPKDPPLKTKV--LDWSQVYIAELQVSDMSFSELSLTYLRISHN-----R 87
Db 88 HLPPEIGQDLKENTLVYQNNLTGVLPKEALATSLKALINSHVPSGHPGQIILPMTK 147
Qy 88 IQLLDL-----SVKFNQDLEYLDLSHN 110
Db 148 LEVLVDYDNNFTGRLPVELVKLEKTKYLKLDGNYFSSGISPSYSSEFK--SLFPLSLSTN 204
Qy 111 QIQ-KI--SCHPIVSFRPHLDSFNDKALPICKEFGNISQLNFLGLSAMKLOKLDLPLTA 167
Db 205 SLSGKPKSKLSKTKTLYLKLGYNNAYEGGIPPEPGSKMSRYLDLSSCNLSG----- 257
Qy 168 HHLSTYLLDLRYVYIKENETESIQILN-AKTLHLVHFPTSLFALQVNI SVNTLGLQLT 226
Db 258 --EIPPSLANLNL-----DILFLQINNLTGTI-----PSELISAM--VSLMSL----- 296
Qy 227 NIKLNDNCOVPIFKPLSELTRGSLTNFTLNHIETWKLCLVRFOFLMPKPYEINLYNL 286
Db 297 DLSINDLQGEIPIPSF-SQL-RNLTLNMFQNNLGS-----VPSFVGEIP----- 339
Qy 287 TIIESIREEDFTYSKTTLKALTIETHTNQVELFSQATALYVSENNIMMLTISDTPFIHM 346
Db 340 -----NLFTLQMDNNFSPV 354
Qy 347 LCPHABST--FKTLNTQNVF-----TDSTFE-----KCSITV 377
Db 355 LPPNLGQNGKLEKFDVIAKNHFTGLIPDLCKSGRLQTIMIDNFRGPIPNEIGNCKSLT 414
Qy 378 KLETLILQKNGL--KDLFKVGLMTKQMPSEILVSNLSL-----SGRHKNCTWYE 428
Db 415 KIRASNNYLVNGVPSGIFK-----LPSTYIIELANNRFGELPPEISG-----E 458
Qy 429 STIVNLNLSNNMLTDSVFRCLPPRIK-----VLDLHSNK-IKSVKQYVVKLEALQELNYA 481
Db 459 SLGILTLNNLFSGKI---PPALKNLRALQTLSTLDANEFGEIVGFDLPMLTVYNIS 514
Qy 482 FNSLT-----DL-----FGCSFSSLSVLIIIDHNSVSHSADPF 515
Db 515 GNNLFGPIPTTLTRCVSLTAVDLSRNNMELGKIPGKIKNLTDLISFNVAISNOISGVPBEI 574
Qy 516 OSCQKMRISIKAGNPFQCTCELREFFVKNIDV-----SSEVLBQMPD---SYKCY 563
Db 575 RMLSLITTLDSNNNF-----IGNVPPGGQRAVSEKSPAGNPNICSHSCN 622
Qy 564 PPSYRGSPLKDFH--MSELSCNITLLIVTIGATMLVLAVTYSLCTIYLDPWYLRMVCW 621
Db 623 SSLYPDDALKRRGRGPMSTKSTRVIVIAIAGTAAIVLAVTYVM----- 666
Qy 622 TOTRRARANI---PLEELQRNLOFHAFISVSEHDSAMVSKELVYLEKEDIQICLHREN 677
Db 667 ---RRKKNNLAKTWKLTAFOR-LNFKA-----EDVVECLKEEN 700

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Oy      678 FVP-----GSIYENIINC1---692
Db      701 IIGGAGAGIYRSGMPNGTDAVALRQLVGAGSGRNDYCFKAIEITLGIKIRRRNRRLGLGY 760
Oy      693 --EKSYKSIYFVLSNFEVQSEWCH-----YE-----LYFAHN-----LFHE 726
Db      761 SNKETNLLILVEYPMNGSLGEMTLGAKGSHLKWEMRYRIYAFAKAGLCYLHHDCSPLIHR 820
Oy      727 G--SNMLIL 733
Db      821 DVKSNMILL 829

RESULT 8
garp precursor - human
C|Species: Homo sapiens (man)
C|Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C|Accession: S42799; I37407
R|Birbaum, D.
Submitted to the EMBL Data Library, July 1993
A|Reference number: S42799
A|Accession: S42799
A|Status: Preliminary
A|Molecule type: mRNA
A|Residues: 1-662 <BIR>
A|Cross-references: UNIPROT:Q14392; UNIPARC:UPI000012B0DF
R|Ollandorff, V.; Noguchi, T.; delapeyriere, O.; Birbaum, D.
Cell Growth Differ. 5, 213-219, 1994
A|Title: The GARP gene encodes a new member of the family of leucine-rich repeat-containing
A|Reference number: I37407; MUID:94235567; PMID:8180135
A|Accession: I37407
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: mRNA
A|Residues: 1-662 <RES>
A|Cross-references: UNIPARC:UPI000012B0DF; EMBL:Z24680; NID:G439295; PIDN:CAA80847.1; PIDN:CAA80847.2
C|Genetics:
A|Gene: GDB:GARP; D11S833E
A|Cross-references: GDB:433911
A|Map position: 11q13.5-11q14
F|50-73/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F|74-97/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F|98-121/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F|125-148/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F|150-173/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F|174-197/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F|198-218/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F|219-242/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F|244-265/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F|266-289/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F|318-339/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F|340-363/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F|364-386/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F|387-410/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F|411-433/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F|444-466/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F|467-490/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F|492-514/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F|515-536/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
F|537-560/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR20>

Query Match      57% Score 238; DB 2; Length 662;
Best Local Similarity 22.4%; Pred. No. 7.7e-08;
Matches 159; Conservative 91; Mismatches 267; Indels 192; Gaps 29;

Oy      17 IMIIVGTRIQFSDGNEF-AVDKSKR---GLIHVPKDLPLKTKVLDMGQNTYIAELQVSD 71
Db      9 LALLITGLIAAQHQDVKPKCKWVDKKVSCQVGLGLQVSPVLPPTETLIDLSGNQIRSLIASP 68
Oy      72 MSFSLSELYTVLRSLSHNRQLDLDSVFKEKNODLEFLDLSHNOLOKISC-----HPYVSFRH 125
Db      69 LGEFTVALRRHLSDLSSTNELSPFQPGAFALTHLEHLSAHHRLAAATKLSAGGLGCLPRVTS 128

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QY 644 AFISYSEHDSAMVKSLEVPYLEKEDIQICLHERNFPEKSIVENI--INCIEKSYKSFIV 701
||| ||| : :
Db 744 -----TSEL--YLESNEIEOIHIER-----IRHRKRSTRDLSSNNOTTI 780

C/Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein	C/Keywords: alternative splicing; growth factor
F166-91/Domain: proteoglycan amino-terminal homology <PAH1>	
F101-134/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>	
F125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>	
F149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>	
F179-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>	
F197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>	
F128-272/Domain: proteoglycan amino-terminal homology <PC1>	
F128-313/Domain: proteoglycan amino-terminal homology <PC2>	
F132-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>	
F137-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>	
F1371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>	
F1395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>	
F1413-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>	
F1450-494/Domain: proteoglycan amino-terminal homology <PC52>	
F1512-537/Domain: proteoglycan amino-terminal homology <PC3>	
F1547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>	
F1572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>	
F1566-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>	
F1620-663/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>	
F1651-695/Domain: proteoglycan amino-terminal homology <PC3>	
F1708-733/Domain: proteoglycan amino-terminal homology <PC4>	
F1748-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>	
F1767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>	
F1791-814/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>	
F1815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>	
F1846-890/Domain: proteoglycan carboxyl-terminal homology <PC34>	
F1028-1051/Domain: EGF homology <EGF>	
F1068-1099/Domain: EGF homology <EGF>	
F1115-1148/Domain: EGF homology <EGF1>	

Query Match 5.6%; Score 233; DB 2; Length 1480;
 Best Local Similarity 18.9%; Pred. No. 4.7e-07;
 Matches 170; Conservative 112; Mismatches 233; Gaps 31;

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Db      84 VDCSHRGLTGVSYPKRSADVERLELQGNMLTVYETDFQRLTGLRMLOLTDNQIHTIERNS 143
Qy      96 EKNPNODELYLDLSHQLOKISCHP-----VSPFHLDLSNDFPALICKEFGNLSQNLFLG 152
Db      144 FODLVSERLDISNNVITTVGRRVFKGASQSLQDLDDNQITC-----LDSHAFRG 194
Qy      153 LSAMKLGQLDLPLFIAHLHLSYLLDLRNYVIKENETESQIOLNAKTLHLVFPHTSLFAIQ 212
Db      195 L-----VELEILTANNNNLTSIPHNIF----- 216
Qy      213 VNISVNTGCTQLINIKLNDNCQVFIKFLSELTEGST-LNLFNTNHIETTKCLVRRVQ 271
Db      217 -----GGIGRLRALSLSDNPFACDCHLSWLSRFLSARFLAPYT-----RCOS----- 259
Qy      272 FLMPKPVYLYNTVNTLITISIREDEFTYKTLKA----- 306
Db      260 ---BSQLKGQNVAD-----HDQFKCSGLTEHAPMECGAENSCPHRCADGVDCRE 310
Qy      307 -----LTIEHITNOVELFSQALYTVFSENNIMMLTISDPTFIMLCFPAHSTFKPL- 358
Db      311 KSLTSVPTLPPDITDVL-----EQN-----FITELPKSFSFRRRLR 349
Qy      359 --NFTQNVPTDSIFPKCSTLVKLETLIQQNGLKDL---FVGLMT----- 399
Db      350 RIDLSNNNISRIAHDAISGLKQTLVLVGNKIKDLPQGVFK-GIGSLRLILNANEISIC 408
Qy      400 -----KMPSEILDVGNLSLES----- 417
Db      409 IRKDAFRDLHSLSLSLYDNNIQLANGTFDAMKSNKTVHLAKNPICDCLMLADYIH 468
Qy      418 -----GRHKENCTWVESIVLVN----- 434
Db      469 KNPISGARGCSPKRMHRRRIESLREEKFKCSWGLMKLSGECRMOSDCPAMCHCEGT 528
Qy      435 -----LSSNML-----TDSVFRCLPPRIKYLDLHNSKIKSY- 465
Db      529 TVDCTGRRLKEIPRDIPLHTTELLINDNELGRISSDGLFGRLLPHLYK-LELKRNLQLTGIE 587
Qy      466 PKQVVKLEALQELNANFNSLTDLPG--CSPFSSSLVLIIDHNSVSPADFPQSOQKMS 523
Db      588 PNAFEGASHIOELQGENEKIKESINMKMELGHLQTLKTLNLYDNOICVMPGSETEHLSLTS 647
Qy      524 IKAGNPFOCTCELEEFVNIQDQVSEVLEGPDSYKCDYPSYSGSPKPKDFHMSLSCN 583
Db      648 LNLASNPNCNCHLAMPACVAKKS---LNG--GARGCAPSKADVOIKDLPHSEPKKS 702
Qy      584 ITLLIVTIGATMLVLAIVTSLCIYLDLPWYLRMVCQMTQTRRANIPLEELQRLNLOFH 643
Db      703 SENSEGCLGDGYCPSCTCTGTIV-----ACSRNQLKEIPRGIAPAE----- 743
Qy      644 AFISISEHDSAMVSELYLEKEDIQICLHERNPVPGSIYENT--INCIEKSYKSYFV 701
Db      744 -----TSEL-----YLESNELBOIHYER-----IRHRSKLRDLDSNNQIT 780
Qy      702 LSPNFVQSEWCHYELVFAHNLFLH-----GSSNNLILILEPIQNSIP-NKYHKLKA 753
Db      781 LS-NTFANLTKLSTLIISYKLCQCLQRALSGLNNLRVLSLHGRLISMPLPGSPEDLKS 839
Qy      754 L 754
Db      840 L 840

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RESULT 12

B66234
 Hypochemical protein [imported] - Arabidopsis thaliana
 CSpecies: Arabidopsis thaliana (mouse-ear cress)
 CDate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #ext_change 31-Dec-2004
 CAccession: B66234
 RTheologos, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
 A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucero, J.S.; Maltli, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A66141; MUID:21016719; PMID:11130712
 A:Accession: B66234
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-921 <STO>
 A:Cross-References: UNIPROT:O04517, UNIPARC:UPI0000048210, GB:AEO05172, NID:g2160189, PI
 C:Genetics:
 C:Map position: 1
 C:Superfamily: Receptor-like protein kinase

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Query Match      5.5%; Score 230.5; DB 2; Length 921;
Best Local Similarity 21.5%; Pred. No. 3.7e-07;
Matches 172; Conservative 137; Mismatches 317; Indels 175; Gaps 39;

Qy      50 LPLKTKVLDMSQNYIAELQVGDMSFL-SELTVLRLSHNRIOQLDLSVFEKNODELYDLS 108
Db      35 LKLASSPAD-----SNLAVFDSWKLNSEALQRL-----ISLV-----ESLEKSLG 76
Qy      109 HNOLOKI-----SCHPIVSFRHLDSFNDER-ALPICKERGNLSQNLFLGISAMKLOKL 161
Db      77 FNSLSGLIPSDLKNC---TSLKYLDLGNLPSGAF--EFSISNQLOFLYIINNSAFS-- 128
Qy      162 DILPFAH--LSYLLDLRNYVIKENETESQIOLNAKTLHLVFPHTSLFAIQNVISVT 219
Db      129 GVFPWKSIRNATSLVLSLGNPDPADAPFPEVVSLSKLSWLYSNCISIGKIPPAIGD 188
Qy      220 LGCLOLTNIKLNDNCQVFIKFLSELTRGSTLNTFNTNHIETTKCLVRRVQFLMPKPE 279
Db      169 L--TELRLHETSDSLTEIP--SEISKLTLMQELVNNLSLTGL-----PTG 233
Qy      280 YLNIYNTLIE---SIREDEFTYKTLKALTEHITNOVELFS-----QT 322
Db      224 FGNLNLTYLDASTVLLQGLSELRLSTNLVLSLQWFEN--FSGEIPLERGEFQDLVNL 290
Qy      323 ALYT--VSENNIMMLTISDPTF---HMLCPHAP-----STPKFLNFTQNVPTDSIF 370
Db      291 SLVTKKLQSGSPQGGSLADPFDIDASENLLTGPIPPMCKKNGKAKALLQNNLTGSI 350
Qy      371 EKCSLTVKLETLIQQNGLKDLFKVGLTKMPSLELDVSNLSLEGRHKENCTWVESI 430
Db      351 ESYANCLTLQFRVSENNLNGTVPAGLW--GLPKLEITDIEMNPF--GPITADINKGML 407
Qy      431 VLNLSNMLTDSVFRCLPPRI-----KVLDSHNSKIK-SVPKQVVKLEALQELNANF 483
Db      408 GALVYGFNKLSD--LPEBIGDTESLTKVELANNRFTGKIPSGIKLKGSLSKMQSN 463
Qy      484 SLT-DLP-GCGSFSSSLVLIIDHNSVSPADFPQSOQKMSIKAGDNP--QCTCEURE 539
Db      464 GFSGEIPDSIGSCMLSDVNAQNSISEIPIHTLGSPLTALNLSIDNKLSGRPESLSS 523
Qy      540 FVKNIQDQVSEVLEGPDSYKCDYPSYSGSP-----LKDPH-----MSELSCNITLL 587
Db      524 LRLSLDLSNNRLSRIPLSLSTYSGNPNGLCSTTIKSPNRCINSRSGIDRRVYL 583
Qy      588 IVTIGATMLVLAIVTSLCIYLDLPWYLRMVCQMTQTRRANIPLEELQRLNLOFHAFIS 647
Db      584 CIVFG-----LLILLASLVFL---YLKLT-----EKKEGSL----- 613
Qy      648 VSEHDSAMVSELYLEKEDIQICLHERNPV-----PGSIYENTINC-- 691
Db      614 --KHESWSIKSFRKMSFTEDDIIDIKENLIGRGCGDYYRVVLVGDGEVAVKHIRCS 671
Qy      692 IEKSYKSYF-VLSPFVQSEWCHYELV---FAHNLF---HEGSSNNLILILEPIPON 742
Db      672 TOKNFSAMPILTEREGSKETETEVQTLSSIRHLNVKLYCISITSDSSSLVETLPLNG 731

```


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OM protein - protein search, using sw model

Run on: June 2, 2006, 22:52:45 ; Search time 107 Seconds
(without alignments)
3401.348 Million cell updates/sec

Title: US-10-732-796a-12

Perfect score: 4154

Sequence: 1 MTKDEPIVSKSFHVCMLMI.....IPAAFMKLTLYENNIVKS 796

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	4154	100.0	796	ADP56660	Adp56660 Human Tol
2	4154	100.0	796	ADP48601	Adp48601 Human Tol
3	4154	100.0	796	ADU23189	Adu23189 Human Tol
4	4149	99.9	796	AAE16109	AAe16109 Human DNA
5	4149	99.9	796	ADU23188	Adu23188 Human Tol
6	4149	99.9	796	ADU23190	Adu23190 Human Tol
7	4149	99.9	796	ADX06216	Adx06216 Cyclin-de
8	4143	99.7	796	AAE18054	AAe18054 Human Tol
9	4048	97.4	780	AAE16112	AAe16112 Human DNA
10	4021	96.8	781	AAU25469	AAu25469 Human mdd
11	3144.5	75.7	795	ADU23197	Adu23197 Murine To
12	3144.5	75.7	806	ADU23195	Adu23195 Murine To
13	3139.5	75.6	806	AAE88055	AAe88055 Murine To
14	3139.5	75.6	806	ADU23194	Adu23194 Murine To
15	3138.5	75.6	806	ADU23196	Adu23196 Murine To
16	2830	68.1	786	AAW86349	AAw86349 Human DNA
17	2830	68.1	786	AAE16090	AAe16090 Human DNA
18	2830	68.1	786	ADU23197	Adu23197 Human PRO
19	2830	68.1	786	ADU23195	Adu23195 Human PRO
20	2830	68.1	786	ADP56650	Adp56650 Human Tol
21	2830	68.1	786	ADP48591	Adp48591 Human Tol
22	2830	68.1	786	ADP54896	Adp54896 Human PRO
23	1905.5	45.9	811	AAy05868	AAy05868 Human Tol

24	1905.5	45.9	811	3	AAy66644	Membrane-
25	1905.5	45.9	811	4	AAU92230	Human PRO
26	1905.5	45.9	811	4	AAE65167	Human PRO
27	1905.5	45.9	811	5	AAE16108	Human DNA
28	1905.5	45.9	811	6	ABU58606	Human PRO
29	1905.5	45.9	811	6	ABU88154	Novel hum
30	1905.5	45.9	811	6	ABU84469	Human sec
31	1905.5	45.9	811	6	ABR66343	Human sec
32	1905.5	45.9	811	6	ABR65733	Human sec
33	1905.5	45.9	811	6	ABU99673	Human sec
34	1905.5	45.9	811	6	ABU57982	Human PRO
35	1905.5	45.9	811	6	ABU59060	Novel hum
36	1905.5	45.9	811	6	ABU82572	Human sec
37	1905.5	45.9	811	6	ABU82912	Human PRO
38	1905.5	45.9	811	6	ABU90033	Novel hum
39	1905.5	45.9	811	6	ABR68282	Human sec
40	1905.5	45.9	811	6	ABU60491	Human sec
41	1905.5	45.9	811	6	ABU96335	Novel hum
42	1905.5	45.9	811	6	ABU92766	Human sec
43	1905.5	45.9	811	6	ABO08843	Human sec
44	1905.5	45.9	811	6	ABO02895	Human sec
45	1905.5	45.9	811	6	ABR75049	Human sec

ALIGNMENTS

RESULT 1
ID ADP56660
ADP56660 standard; protein; 796 AA.
XX
AC ADP56660;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human Toll-like receptor TLR6 protein - SEQ ID 12.
XX
KW expression system; Toll-like receptor; TLR6; immune response modifier;
KW IRM; cancer; gene therapy; human; receptor.
XX
OS Homo sapiens.
XX
PN MO2004053057-A2.
XX
PD 24-JUN-2004.
XX
PF 31-OCT-2003; 2003WO-US034563.
XX
PR 11-DEC-2002; 2002US-0432651P.
XX
(MINN) 3M INNOVATIVE PROPERTIES CO.
XX
Gupta SK, Ghosh TK, Fink JR;
XX
WPI: 2004-468833/44.
XX
N-PSDB: ADP56659.
XX
PT New expression system comprising a first nucleic acid sequence that
XX encodes a Toll-like receptor (TLR), useful for preparing a composition
XX comprising TLR agonist for treating e.g., cancer.
XX
PS Claim 4; SEQ ID NO 12; 69pp; English.
XX
The invention relates to a novel expression system comprising a first
XX nucleic acid sequence that encodes a Toll-like receptor (TLR) operably
XX linked to a first expression control sequence and a second nucleic acid
XX sequence that encodes a reporter. TLRs are immune response modifiers
XX (IRMS). The expression system of the invention may be useful for
XX preparing a composition comprising the TLR agonist for treating cancer,
XX possibly via gene therapy. The current sequence is that of the human Toll
XX -like receptor TLR6 protein (SEQ ID 12) of the invention.
SQ Sequence 796 AA;

Query Match 100.0%; Score 4154; DB 8; Length 796;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MTKDKEPIVKSFPHFVCLMIIIVGTRIOFSDGNEFVADSKRGLHVPKDLPIKTVLDM 60
DB 1 MTKDKEPIVKSFPHFVCLMIIIVGTRIOFSDGNEFVADSKRGLHVPKDLPIKTVLDM 60
QY 61 QNYIAELQVSDMSFSELTIVRLSHNRIOQLDLSVFKENODLEYLDLSHNOLOKISCHPI 120
DB 61 QNYIAELQVSDMSFSELTIVRLSHNRIOQLDLSVFKENODLEYLDLSHNOLOKISCHPI 120
QY 121 VSFRLDLSFNDFKALPICKERGNLSQNLFLGLSAMKLOKDLPIAHLSYILLDRN 180
DB 121 VSFRLDLSFNDFKALPICKERGNLSQNLFLGLSAMKLOKDLPIAHLSYILLDRN 180
QY 181 YIKENETESLOINAKTLHLVHPTSLFAIOVNSVNTLGCLQTLNKLKANDNCQVFIK 240
DB 181 YIKENETESLOINAKTLHLVHPTSLFAIOVNSVNTLGCLQTLNKLKANDNCQVFIK 240
QY 241 FLSELTGRSTLINFNLNIEETWKCLVRFQFLMKPEYLNINVLTIIESIREDFYIS 300
DB 241 FLSELTGRSTLINFNLNIEETWKCLVRFQFLMKPEYLNINVLTIIESIREDFYIS 300
QY 301 KTTLKALTIETHTNOVFLFSQALYTVFSENNIMMLTISDTPFIHMLCPHAPSTFKFLNF 360
DB 301 KTTLKALTIETHTNOVFLFSQALYTVFSENNIMMLTISDTPFIHMLCPHAPSTFKFLNF 360
QY 361 TQNVFTDSIFEKCSFLVKLETLILQKNGIKDI.FKVGMLTKMDPSEILDVSNLSGSRH 420
DB 361 TQNVFTDSIFEKCSFLVKLETLILQKNGIKDI.FKVGMLTKMDPSEILDVSNLSGSRH 420
QY 421 KENCWWSIVVNLSSNNMLTDSVRCCLPBRITKVIDLSHNRKISVPKQVVKLEALQELNV 480
DB 421 KENCWWSIVVNLSSNNMLTDSVRCCLPBRITKVIDLSHNRKISVPKQVVKLEALQELNV 480
QY 481 AFNSLTDLPGCGSFSSLSVLIIDHNSVSHPSADFPQSCQKMSIXAGDNPFQCTCELRF 540
DB 481 AFNSLTDLPGCGSFSSLSVLIIDHNSVSHPSADFPQSCQKMSIXAGDNPFQCTCELRF 540
QY 541 VKNIDQVSSEVLKGPDSYKCDYPPSYRSGSLKDFHMSLSNLTLLYTTGATMLVLAV 600
DB 541 VKNIDQVSSEVLKGPDSYKCDYPPSYRSGSLKDFHMSLSNLTLLYTTGATMLVLAV 600
QY 601 TWTSLCTIYLDLPWYLRMVCQWOTQTRRARNIPLEBELQRLQPHAFISYSEHDSAWKSEL 660
DB 601 TWTSLCTIYLDLPWYLRMVCQWOTQTRRARNIPLEBELQRLQPHAFISYSEHDSAWKSEL 660
QY 661 VPYLEKEDIQICLHERNFVPGKSIENINICIEKSYKSI.FVLSPNFVQSEWCHYELYPFH 720
DB 661 VPYLEKEDIQICLHERNFVPGKSIENINICIEKSYKSI.FVLSPNFVQSEWCHYELYPFH 720
QY 721 HNLFEHGSNNLLILLEPIPNKHYKALKALMTORTYLOWPEKSKRGIFANIRAA 780
DB 721 HNLFEHGSNNLLILLEPIPNKHYKALKALMTORTYLOWPEKSKRGIFANIRAA 780
QY 781 FNMKLTIVTENNDVKS 796
DB 781 FNMKLTIVTENNDVKS 796

RESULT 2
ADP48601 standard; protein; 796 AA.
ADP48601;
ADP48601;
09-SEP-2004 (first entry)
Human Toll-like receptor 6 protein SEQ ID NO:12.
Toll-like receptor; TLR; human; detection; identification; TLR agonist;

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```

KW TLR antagonist; Toll like receptor 6; TLR6; chromosome 4.
XX
XX Homo sapiens.
XX WO2004053452-A2.
XX
XX 24-JUN-2004.
XX
XX 31-OCT-2003; 2003WO-US034554.
XX
XX 11-DEC-2002; 2002US-0432650P.
XX
XX (MINN ) 3M INNOVATIVE PROPERTIES CO.
XX
XX Gupta SK, Ghosh TK, Fink JR;
XX WPI: 2004-468955/44.
XX N-PSDB; ADP48600.
XX
XX Detecting activation of Toll-like receptors (TLR) for identifying a TLR
XX agonist or antagonist, comprises providing a cell culture comprising
XX cells transfected with a sequence encoding a reporter.
XX
XX Claim 8; SEQ ID NO 12; 78bp; English.
XX
XX The present invention describes a method for detecting activation of a
XX Toll-like receptor (TLR) in a cell. The method comprises: (a) providing a
XX cell culture comprising cells transfected with a nucleic acid sequence
XX that encodes a reporter that (i) generates a detectable signal when the
XX reporter is expressed and the cell is exposed to conditions for
XX generating the detectable signal, and (ii) is operably linked to an
XX expression control sequence that is induced by activation of a TLR and
XX comprises a cytokine promoter, a chemokine promoter, a co-stimulatory
XX marker promoter, or a defense promoter; (b) exposing the cell culture to
XX a compound that activates a TLR; (c) providing conditions for generating
XX the detectable signal, and (d) detecting the detectable signal. Also
XX described: (1) a method of identifying a TLR agonist or antagonist; (2) a
XX TLR agonist or antagonist identified by the method of (1); and (3) a
XX pharmaceutical composition comprising a TLR agonist or antagonist
XX identified by the method of (1) and a pharmaceutical salt. The methods
XX are useful for detecting activation of a TLR in a cell and for
XX identifying TLR agonist or antagonist. The present sequence represents a
XX human TLR6 which is used in the exemplification of the present invention.
XX The human TLR6 gene is located on chromosome 4, more specifically to
XX 4p14.
XX
XX Sequence 796 AA;
XX
XX Query Match 100.0%; Score 4154; DB 8; Length 796;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTKDKEPIVKSFPHFVCLMIIIVGTRIOFSDGNEFVADSKRGLHVPKDLPIKTVLDM 60
DB 1 MTKDKEPIVKSFPHFVCLMIIIVGTRIOFSDGNEFVADSKRGLHVPKDLPIKTVLDM 60
QY 61 QNYIAELQVSDMSFSELTIVRLSHNRIOQLDLSVFKENODLEYLDLSHNOLOKISCHPI 120
DB 61 QNYIAELQVSDMSFSELTIVRLSHNRIOQLDLSVFKENODLEYLDLSHNOLOKISCHPI 120
QY 121 VSFRLDLSFNDFKALPICKERGNLSQNLFLGLSAMKLOKDLPIAHLSYILLDRN 180
DB 121 VSFRLDLSFNDFKALPICKERGNLSQNLFLGLSAMKLOKDLPIAHLSYILLDRN 180
QY 181 YIKENETESLOINAKTLHLVHPTSLFAIOVNSVNTLGCLQTLNKLKANDNCQVFIK 240
DB 181 YIKENETESLOINAKTLHLVHPTSLFAIOVNSVNTLGCLQTLNKLKANDNCQVFIK 240
QY 241 FLSELTGRSTLINFNLNIEETWKCLVRFQFLMKPEYLNINVLTIIESIREDFYIS 300
DB 241 FLSELTGRSTLINFNLNIEETWKCLVRFQFLMKPEYLNINVLTIIESIREDFYIS 300
QY 301 KTTLKALTIETHTNOVFLFSQALYTVFSENNIMMLTISDTPFIHMLCPHAPSTFKFLNF 360

```


ID AAE16109 standard; protein; 796 AA.
 AC AAE16109;
 XX
 XX 26-MAR-2002 (first entry)
 DE Human DNAX Toll like receptor (DTLR) 9 #2.
 XX
 XX Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
 KM interleukin 1; IL-1; screening; immunomodulator.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..31
 FT /label= Signal_peptide
 FT Protein 32..796
 FT /note= "Human mature DTLR9"
 FT Region 549..582
 FT /note= "Transmembrane segment"
 FT
 XX WO200190151-A2.
 XX 29-NOV-2001 ✓
 XX 23-MAY-2001; 2001WO-US016766.
 XX 25-MAY-2000; 2000US-0207558P.
 XX (SCHE) SCHERING CORP.
 PA Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
 PI WPI; 2002-083085/11.
 XX N-PSDB; AAD26300.
 DR
 XX New DNAX Toll like receptor (DTLR) proteins, useful for treating
 PT conditions exhibiting abnormal expression of the receptors of their
 PT ligands, particularly abnormalities manifested by immunological
 PT disorders.
 PT
 XX Claim 1; Page 76; 297pp; English.
 PS The invention relates to mammalian receptor proteins, e.g., primate,
 XX human DNAX Toll like receptor (DTLR) protein and their corresponding
 CC nucleic acids. The DTLR is useful for treating conditions exhibiting
 CC abnormal expression of the receptors of their ligands. Such abnormality
 CC is manifested by immunological disorders. In particular, the DTLR is
 CC useful for treating various disease or disorders associated with abnormal
 CC expression or abnormal triggering of response to a ligand. The DTLR is
 CC also useful as an immunogen for the production of antisera or antibodies
 CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
 CC receptor family members, for the DTLR or its various fragments. The
 CC purified DTLR can be used to screen monoclonal antibodies or antigen-
 CC binding fragments. The antibodies are useful for screening expression
 CC libraries for particular expression products. These are useful for
 CC detecting or diagnosing various immunological conditions related to
 CC expression of DTLR or cells that express it. The present sequence is
 CC human DTLR9 protein
 XX
 SQ Sequence 796 AA;
 Query Match 99.9%; Score 4149; DB 5; Length 796;
 Best local similarity 99.9%; Pred. No. 0;
 Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MTKDKKPIVKSFFVCLMIIIVGTRIQFSDGNEFAVDKSKRGLIHVPKDLPLKTKVLDMS 60
 DB 1 MTKDKKPIVKSFFVCLMIIIVGTRIQFSDGNEFAVDKSKRGLIHVPKDLPLKTKVLDMS 60
 QY 61 QNYIYELQVSDMSFISELTVLRLSHNRITQLDLISVKKFQDDELYDLISNOLQKISCHPI 120
 DB 61 QNYIYELQVSDMSFISELTVLRLSHNRITQLDLISVKKFQDDELYDLISNOLQKISCHPI 120

QY 121 VSPRHLDLSPNDPKALPICKFEGNLSQLNPLGLSAMKLOKLDLLPIAHLHSYLLDLRN 180
 DB 121 VSPRHLDLSPNDPKALPICKFEGNLSQLNPLGLSAMKLOKLDLLPIAHLHSYLLDLRN 180
 QY 181 YIKENETESQIINAKTIHLVFFHPTSLFAQVNIISVNTIGCLOLTNKLKNDNCOVFIK 240
 DB 181 YIKENETESQIINAKTIHLVFFHPTSLFAQVNIISVNTIGCLOLTNKLKNDNCOVFIK 240
 QY 241 FLSLSTRGSTLLNPLNHIETTWKCLVRVFOFLPKPKVEYLINVLNLTIESIREDFYTS 300
 DB 241 FLSLSTRGSTLLNPLNHIETTWKCLVRVFOFLPKPKVEYLINVLNLTIESIREDFYTS 300
 QY 301 KTKLALTIETHTNQVLPFSQTALYTVPSSENNIMLTI SDTPFIHMLCPHAPSTFKPLNF 360
 DB 301 KTKLALTIETHTNQVLPFSQTALYTVPSSENNIMLTI SDTPFIHMLCPHAPSTFKPLNF 360
 QY 361 TQNVFTDSIFPKGKSTVYKLETLIIQKNGKDLFFVGLMTKMPBLEILDVSNLSGGRH 420
 DB 361 TQNVFTDSIFPKGKSTVYKLETLIIQKNGKDLFFVGLMTKMPBLEILDVSNLSGGRH 420
 QY 421 KENCTWVESIVVLNLSNMLTDSVFRCLPPIIKVLDLSNKKIKSVKQVVLALQELNV 480
 DB 421 KENCTWVESIVVLNLSNMLTDSVFRCLPPIIKVLDLSNKKIKSVKQVVLALQELNV 480
 QY 481 AFNSITDLPGGGSFSSLSVLLIIDHNSVSHPSADFPQSCQKRSIKAGDNPQCTCELRFP 540
 DB 481 AFNSITDLPGGGSFSSLSVLLIIDHNSVSHPSADFPQSCQKRSIKAGDNPQCTCELRFP 540
 QY 541 VKNIDQVSEVLEGPDSYKCDYPSYRGSPLKDFHSELSCNTLLIVTIGATMLVLA 600
 DB 541 VKNIDQVSEVLEGPDSYKCDYPSYRGSPLKDFHSELSCNTLLIVTIGATMLVLA 600
 QY 601 TVTSICITLDLPWYLRMCQWOTRRRARNPILBELQNLQFPAFISYSEHDSAMVXSEL 660
 DB 601 TVTSICITLDLPWYLRMCQWOTRRRARNPILBELQNLQFPAFISYSEHDSAMVXSEL 660
 QY 661 VPLYEKEDIQICLHERNFVPGKSIIVENIINCIEKSYKSI FVLSNPFVQSEKCHYELFAH 720
 DB 661 VPLYEKEDIQICLHERNFVPGKSIIVENIINCIEKSYKSI FVLSNPFVQSEKCHYELFAH 720
 QY 721 HNLPHGSGNNLILILEPIPNQSTIPNKYHKLKALMTQRTYQWPEKSKRGLFWANIRAA 780
 DB 721 HNLPHGSGNNLILILEPIPNQSTIPNKYHKLKALMTQRTYQWPEKSKRGLFWANIRAA 780
 QY 781 FNMKLTLYTENNDVKS 796
 DB 781 FNMKLTLYTENNDVKS 796
 RESULT 5
 ADU23188
 ID ADU23188 standard; protein; 796 AA.
 AC ADU23188;
 XX 27-JAN-2005 (first entry)
 DE Human Toll-like receptor 6 (TLR6) protein - SEQ ID 80.
 XX
 XX screening; Toll-like receptor agonist; TLR agonist; TLR6.
 KM Homo sapiens.
 OS
 XX
 XX WO2004094671-A2.
 XX 04-NOV-2004.
 PD 22-APR-2004; 2004WO-US012788.
 PF 22-APR-2003; 2003US-0464586P.
 PR 22-APR-2003; 2003US-0464586P.
 XX


```
Db 121 VSRHLDLSPNDFKALPICKFEGNISQNLFLGLSANKLOKDLPLIAHLHSYILLDRN 180
Qy 181 YYIKENETESLQIINAKTLHLVHFPTSLFAIOVINSVNTLGLQLTINIKLNDNCQVFX 240
Db 181 YYIKENETESLQIINAKTLHLVHFPTSLFAIOVINSVNTLGLQLTINIKLNDNCQVFX 240
Qy 241 FLSELTRGSTLLNFTLNHIETTWKCLAVRFOFLMPKPEVYINIVLTTIIESIREDDFTYS 300
Db 241 FLSELTRGSTLLNFTLNHIETTWKCLAVRFOFLMPKPEVYINIVLTTIIESIREDDFTYS 300
Qy 301 KTTLKALITEHTITNOVFLFSQALYTVFSENNIMMLTISDPFIHMLCPHASTFKFLNF 360
Db 301 KTTLKALITEHTITNOVFLFSQALYTVFSENNIMMLTISDPFIHMLCPHASTFKFLNF 360
Qy 361 TONVFTDSIFEKCSLTVLKLETLILQKNGKDLFKVGLMTKMPSEILDVSNNSLESGRH 420
Db 361 TONVFTDSIFEKCSLTVLKLETLILQKNGKDLFKVGLMTKMPSEILDVSNNSLESGRH 420
Qy 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPRIKVLDSLHNSNKIKSVKQVVKLEALQELNV 480
Db 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPRIKVLDSLHNSNKIKSVKQVVKLEALQELNV 480
Qy 481 AFNSLJTDLPGCCSFSSLSVLIIIDHNSVSHPSADFFQSCQKMSIKAGDNPFCCTCELREF 540
Db 481 AFNSLJTDLPGCCSFSSLSVLIIIDHNSVSHPSADFFQSCQKMSIKAGDNPFCCTCELREF 540
Qy 541 VNINIOVSEVLEGMPSYKCDYPESYRGSPLKDFHMSLSGNITLLIYTGATMLVLAV 600
Db 541 VNINIOVSEVLEGMPSYKCDYPESYRGSPLKDFHMSLSGNITLLIYTGATMLVLAV 600
Qy 601 TVTSLCIYIDLPMYLRMVCQMTQTRRRANIPLEBEIQNLQPHAFISYSEHDSAMVKSFL 660
Db 601 TVTSLCIYIDLPMYLRMVCQMTQTRRRANIPLEBEIQNLQPHAFISYSEHDSAMVKSFL 660
Qy 661 VPYLEKEDIQICLHERNFPGKSIYENIINCEKSYKSI FVLSPNVQSEMGCHYEYFHH 720
Db 661 VPYLEKEDIQICLHERNFPGKSIYENIINCEKSYKSI FVLSPNVQSEMGCHYEYFHH 720
Qy 721 HNLFFHGSNNLILILEPIPNISIPKVKHKLKALMTORTYLOMPKEKSKRGFLFMANIRAA 780
Db 721 HNLFFHGSNNLILILEPIPNISIPKVKHKLKALMTORTYLOMPKEKSKRGFLFMANIRAA 780
Qy 781 FNMKLTLYTENNDVKS 796
Db 781 FNMKLTLYTENNDVKS 796

RESULT 7
ADX06216
ID ADX06216 standard; protein; 796 AA.
XX
AC ADX06216;
XX
DT 21-APR-2005 (first entry)
XX
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 781.
XX
KW cytosolic; cyclin-dependent kinase; cdk; biomarker.
XX
OS Homo sapiens.
XX
PN WO2005012875-A2.
XX
PD 10-FEB-2005.
XX
PF 29-JUL-2004; 2004WO-US024424.
XX
PR 29-JUL-2003; 2003US-0490890P.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
```

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DR WPI, 2005-163068/17.
DR N-PSDB; ADX06215.
XX
PT Biomarkers useful for predicting or determining the response of a mammal
PT to a cancer treatment comprising administration of a modulator of cyclin-
PT dependent kinase activity.
XX
PS Claim 5; SEQ ID NO 781; 141pp; English.
XX
XX
CC This invention describes a novel method of predicting or determining
CC whether a mammal will respond or is responding to an anti-cancer agent
CC that modulates cyclin-dependent kinase (cdk) activity. The method
CC comprises measuring the level of one or more biomarkers selected from
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC NO:1246 (Genbank EST W26729) is especially preferred). The method of the
CC invention is utilized in a kit for determining or predicting whether
CC patient would be susceptible or resistant to treatment by an agent
CC modulating cdk activity. The invention also describes a method for
CC utilizing individualized genetic profiles for treating diseases and
CC disorders based on patient's response and molecular level, specialized
CC microarrays comprising the biomarkers described, antibodies directed
CC against the biomarkers and a cell culture model to identify biomarkers.
CC The cdk modulator is preferably N-5-[(5-(1,1-dimethylethyl)-2-
CC oxazolyl)methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
CC tartaric acid salt. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from Wipo at ftp.wipo.int/pub/published.pat.sequences. This
CC sequence represents a biomarker used in the method of the invention.
XX
SQ Sequence 796 AA:
XX
Query Match 99.9%; Score 4149; DB 9; Length 796;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MTKDKEPIVKSFRFCMLITIVGTPIQSPDNGEFAVDSKRGILHVPDLPKTKVLMS 60
Db 1 MTKDKEPIVKSFRFCMLITIVGTPIQSPDNGEFAVDSKRGILHVPDLPKTKVLMS 60
Qy 61 QNYIAELQVSDMSFSELTVALRLSHNRIOQLDLSYFKNODELYDLDSHNOLOKISCHPI 120
Db 61 QNYIAELQVSDMSFSELTVALRLSHNRIOQLDLSYFKNODELYDLDSHNOLOKISCHPI 120
Qy 121 VSRHLDLSPNDFKALPICKFEGNISQNLFLGLSANKLOKDLPLIAHLHSYILLDRN 180
Db 121 VSRHLDLSPNDFKALPICKFEGNISQNLFLGLSANKLOKDLPLIAHLHSYILLDRN 180
Qy 181 YYIKENETESLQIINAKTLHLVHFPTSLFAIOVINSVNTLGLQLTINIKLNDNCQVFX 240
Db 181 YYIKENETESLQIINAKTLHLVHFPTSLFAIOVINSVNTLGLQLTINIKLNDNCQVFX 240
Qy 241 FLSELTRGSTLLNFTLNHIETTWKCLAVRFOFLMPKPEVYINIVLTTIIESIREDDFTYS 300
Db 241 FLSELTRGSTLLNFTLNHIETTWKCLAVRFOFLMPKPEVYINIVLTTIIESIREDDFTYS 300
Qy 301 KTTLKALITEHTITNOVFLFSQALYTVFSENNIMMLTISDPFIHMLCPHASTFKFLNF 360
Db 301 KTTLKALITEHTITNOVFLFSQALYTVFSENNIMMLTISDPFIHMLCPHASTFKFLNF 360
Qy 361 TONVFTDSIFEKCSLTVLKLETLILQKNGKDLFKVGLMTKMPSEILDVSNNSLESGRH 420
Db 361 TONVFTDSIFEKCSLTVLKLETLILQKNGKDLFKVGLMTKMPSEILDVSNNSLESGRH 420
Qy 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPRIKVLDSLHNSNKIKSVKQVVKLEALQELNV 480
Db 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPRIKVLDSLHNSNKIKSVKQVVKLEALQELNV 480
Qy 481 AFNSLJTDLPGCCSFSSLSVLIIIDHNSVSHPSADFFQSCQKMSIKAGDNPFCCTCELREF 540
Db 481 AFNSLJTDLPGCCSFSSLSVLIIIDHNSVSHPSADFFQSCQKMSIKAGDNPFCCTCELREF 540
Qy 541 VNINIOVSEVLEGMPSYKCDYPESYRGSPLKDFHMSLSGNITLLIYTGATMLVLAV 600
Db 541 VNINIOVSEVLEGMPSYKCDYPESYRGSPLKDFHMSLSGNITLLIYTGATMLVLAV 600
```

Db 541 VKNIDQVSEVLEGMWDSYKCDYPSYRGSPLKDFHMSLSGNTITLLIYTGATMLVLAV 600
QY 601 TVTSLCIYLDLPWYLRMCQWOTRRRARNIPLEELQRMLOPHAFISYSEHDSAMWKSSEL 660
Db 601 TVTSLCIYLDLPWYLRMCQWOTRRRARNIPLEELQRMLOPHAFISYSEHDSAMWKSSEL 660
QY 661 VPYLEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSIFFVLSPNFVQSEWCHEYELYPFAH 720
Db 661 VPYLEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSIFFVLSPNFVQSEWCHEYELYPFAH 720
QY 721 HNLFHGSGNNLLIILILEPIPNQSIIPKXHKALKALMTQRTYLOMPKESKRGLEFWANIRAA 780
Db 721 HNLFHGSGNNLLIILILEPIPNQSIIPKXHKALKALMTQRTYLOMPKESKRGLEFWANIRAA 780
QY 781 FNNKLTIVTENNDDVKS 796
Db 781 FNNKLTIVTENNDDVKS 796

RESULT 8

AA88054
ID AA88054 standard; protein; 796 AA.

AC AA88054;

DT 22-SEP-2000 (first entry)

DE Human Toll-like receptor TLR6 protein.

KW Toll-like receptor; TLR6; human; anti-infectious; treatment; infection;
transcription factor; NF-kappaB; immune response.

XX Homo sapiens.

XX WO200024776-A1.

PD 04-MAY-2000.

PF 26-OCT-1999; 99WO-JP005917.

PR 26-OCT-1998; 98JP-00304110.

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PI Akira S, Takeuchi O;

DR WPI; 2000-350697/30.

DR N-PSDB; AAA39809.

PT Toll-like receptor TLR6 molecule and encoded gene, participating in
signal transduction of initial immune response, applicable e.g. in
treating infections.

PS Claim 1; Page 27-29; 35pp; Japanese.

CC This invention describes a novel toll-like receptor TLR6 which has
anti-infectious activity. The protein and its encoded gene have clinical
use e.g. in treating infections. Toll family receptors are related to
transcription factor NF-kappaB and regulate the expression of various
CC genes participating in the immune response. This sequence represents the
human TLR6 protein which is described in the method of the invention
XX
SQ Sequence 796 AA;

Query Match 99.7%; Score 4143; DB 3; Length 796;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 794; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTKDKEPIKSFHFVCLMIIIVGTRIQPSDGNFPAVDKSRGLIHVPKDLPLKTKVLDM 60
Db 1 MTKDKEPIKSFHFVCLMIIIVGTRIQPSDGNFPAVDKSRGLIHVPKDLPLKTKVLDM 60
QY 61 QNYIAELQVSDMSFLSELTVLRISHNRIOQLDLVSFKFNQDLELYDLISHNOLOKISCHPI 120

Db 61 QNYIAELQVSDMSFLSELTVLRISHNRIOQLDLVSFKFNQDLELYDLISHNOLOKISCHPI 120
QY 121 VSFRRHLDLSPNDPKALPIKKEFGNLSQNLFGISAMKLOKDLLPAHLSYIILDLN 180
Db 121 VSFRRHLDLSPNDPKALPIKKEFGNLSQNLFGISAMKLOKDLLPAHLSYIILDLN 180
QY 181 YTIKENETESLOLNKATLHVPHPTSLPAIOVNISVNTGCLQTNIKLANDNCQVFIK 240
Db 181 YTIKENETESLOLNKATLHVPHPTSLPAIOVNISVNTGCLQTNIKLANDNCQVFIK 240
QY 241 FLSLTRGSTLLNFTLNHIETWKCLVRVFOFLMPKRVLYNLNLTIIIESIREEDFTYS 300
Db 241 FLSLTRGSTLLNFTLNHIETWKCLVRVFOFLMPKRVLYNLNLTIIIESIREEDFTYS 300
QY 301 KTTLKALTEIHTNOVFLFSOTALYVSENNIMMLTISDTPFIHMLCPHASTFKFLNF 360
Db 301 KTTLKALTEIHTNOVFLFSOTALYVSENNIMMLTISDTPFIHMLCPHASTFKFLNF 360
QY 361 TQNVFTDSIFEKCSITLVKLETLILQKNGKDLFKVGLMTKMPSEILVSNNSLESGRH 420
Db 361 TQNVFTDSIFEKCSITLVKLETLILQKNGKDLFKVGLMTKMPSEILVSNNSLESGRH 420
QY 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPIRIKVLDSLHNSKITSVPKQVVKLEALQELNV 480
Db 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPIRIKVLDSLHNSKITSVPKQVVKLEALQELNV 480
QY 481 AFNSLTDLPGCSFSSLSVLIIDHNSVSHPSADFPQSCQKMSIKAGDNPFOCTCELRSF 540
Db 481 AFNSLTDLPGCSFSSLSVLIIDHNSVSHPSADFPQSCQKMSIKAGDNPFOCTCELRSF 540
QY 541 VKNIDQVSEVLEGMWDSYKCDYPSYRGSPLKDFHMSLSGNTITLLIYTGATMLVLAV 600
Db 541 VKNIDQVSEVLEGMWDSYKCDYPSYRGSPLKDFHMSLSGNTITLLIYTGATMLVLAV 600
QY 601 TVTSLCIYLDLPWYLRMCQWOTRRRARNIPLEELQRMLOPHAFISYSEHDSAMWKSSEL 660
Db 601 TVTSLCIYLDLPWYLRMCQWOTRRRARNIPLEELQRMLOPHAFISYSEHDSAMWKSSEL 660
QY 661 VPYLEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSIFFVLSPNFVQSEWCHEYELYPFAH 720
Db 661 VPYLEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSIFFVLSPNFVQSEWCHEYELYPFAH 720
QY 721 HNLFHGSGNNLLIILILEPIPNQSIIPKXHKALKALMTQRTYLOMPKESKRGLEFWANIRAA 780
Db 721 HNLFHGSGNNLLIILILEPIPNQSIIPKXHKALKALMTQRTYLOMPKESKRGLEFWANIRAA 780
QY 781 FNNKLTIVTENNDDVKS 796
Db 781 FNNKLTIVTENNDDVKS 796

RESULT 9

AAE16112
ID AAE16112 standard; protein; 780 AA.

AC AAE16112;

DT 26-MAR-2002 (first entry)

DE Human DNAX Toll like receptor (DTLR) 9 #2, alternative version.

KW Human; DNAX Toll like receptor; DTLR, therapy; immunological disorder;
interleukin 1; IL-1; screening; immunomodulator.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide /label= Signal_peptide

FT Protein 32..780
FT /note="Human mature DTLR9"

FT Misc-difference 176..177

FT /note= "Encoded by CTGGATTGAAGAAATATATATATAAAGAA
 FT AATGACAGCAAGTCTCAAAATT"
 FT 549..582
 FT Region /note="Transmembrane segment"
 FT
 EN WO200190151-A2.
 XX
 XX 29-NOV-2001.
 XX
 XX 23-MAY-2001; 2001WO-US016766.
 XX
 XX 25-MAY-2000; 2000US-0207558P.
 XX
 XX (SCHE) SCHERING CORP.
 XX
 XX Hardiman GT, Rock FL, Bazan JF, Kastetelein RA, Ho SWK, Liu Y,
 XX
 XX WPI; 2002-083085/11.
 DR N-PSDB; AAD26300.
 XX
 PT New DNAX Toll like receptor (DTRL) proteins, useful for treating
 PT conditions exhibiting abnormal expression of the receptors of their
 PT ligands, particularly abnormalities manifested by immunological
 PT disorders.
 XX
 PS Claim 1; Page 274-276; 297pp; English.
 XX
 CC The invention relates to mammalian receptor proteins, e.g., primate,
 CC human DNAX Toll like receptor (DTRL) protein and their corresponding
 CC nucleic acids. The DTRL is useful for treating conditions exhibiting
 CC abnormal expression of the receptors of their ligands. Such abnormality
 CC is manifested by immunological disorders. In particular, the DTRL is
 CC useful for treating various disease or disorders associated with abnormal
 CC expression or abnormal triggering of response to a ligand. The DTRL is
 CC also useful as an immunogen for the production of antisera or antibodies
 CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
 CC receptor family members, for the DTRL or its various fragments. The
 CC purified DTRL can be used to screen monoclonal antibodies or antigen-
 CC binding fragments. The antibodies are useful for screening expression
 CC libraries for particular expression products. These are useful for
 CC detecting or diagnosing various immunological conditions related to
 CC expression of DTRL or cells that express it. The present sequence is
 CC human DTRL protein, alternative version. Note: The present sequence SEQ
 CC ID NO 41 is stated to be similar to the sequence shown in page 76
 CC (AAL16109). However these sequences differ at several locations
 CC
 XX
 SQ Sequence 780 AA;
 Query Match 97.4%; Score 4048; DB 5; Length 780;
 Best Local Similarity 97.9%; Pred. No. 0;
 Matches 779; Conservative 0; Mismatches 1; Indels 16; Gaps 1;
 QY 1 MTKDKEPIYKSFHPCVCLMIITVGRIOFSDGNEFAVDKSKRGILHHPKDLPLKTKYLDMS 60
 DB 1 MTKDKEPIYKSFHPCVCLMIITVGRIOFSDGNEFAVDKSKRGILHHPKDLPLKTKYLDMS 60
 QY 61 QNYIAELOVSDMSPISELTFTLRLSHNRIOQLDLVYKFNQDLELYDLISHNOLOKTSCHPI 120
 DB 61 QNYIAELOVSDMSPISELTFTLRLSHNRIOQLDLVYKFNQDLELYDLISHNOLOKTSCHPI 120
 QY 121 VSFRLHDSFNDFKALPICKERGNLSQNLFLGISANKLOKDLPLPAHHLSTYILLDLRN 180
 DB 121 VSFRLHDSFNDFKALPICKERGNLSQNLFLGISANKLOKDLPLPAHHLSTYILLDLRN 180
 QY 181 YIKENETESLOILNAKTLHLVHPPTSLPAIQVNISVNTLGCQLTNKLNNDNCQVFLK 240
 DB 181 YIKENETESLOILNAKTLHLVHPPTSLPAIQVNISVNTLGCQLTNKLNNDNCQVFLK 240
 QY 177 -----ILNAKTLHLVHPPTSLPAIQVNISVNTLGCQLTNKLNNDNCQVFLK 224
 DB 241 FLSELTRGSLTNFNTLNHETTKMCLVRYFOFLMPKPVYINLYNTLTIESTREDFPTS 300
 QY 225 FLSELTRGSLTNFNTLNHETTKMCLVRYFOFLMPKPVYINLYNTLTIESTREDFPTS 284
 DB 301 KTLKALTEIHTNOVFLFSQALVYTFSENNIMMLTISDTPFIHMLCPHASTFEKLNLF 360

DB 285 KTTLKALETIHTNOVFLFSQALVYTFSENNIMMLTISDTPFIHMLCPHASTFEKLNLF 344
 QY 361 TONVFTDSIFEKCSLVLEETLILQKNGIKDLFKVGLMTKMPSEILIDVSNLSGSRH 420
 DB 345 TONVFTDSIFEKCSLVLEETLILQKNGIKDLFKVGLMTKMPSEILIDVSNLSGSRH 404
 QY 421 KENCTWVESIVVLNLSNMULTDSVFRCLPPRIKVLIDHSNKIKSVYKQVVKLEALQELNV 480
 DB 405 KENCTWVESIVVLNLSNMULTDSVFRCLPPRIKVLIDHSNKIKSVYKQVVKLEALQELNV 464
 QY 461 AFNSLTDLPGCGSFSLSVLIIIDHNSVSHPADDFQSCQKRKSIYAGNPFQCTCELEKF 540
 DB 465 AFNSLTDLPGCGSFSLSVLIIIDHNSVSHPADDFQSCQKRKSIYAGNPFQCTCELEKF 524
 QY 541 VNINQVSEVLEGPDSYKCDYPESYSGSLKDFHMSLSNITLLIVTIGATMLVLAV 600
 DB 525 VNINQVSEVLEGPDSYKCDYPESYSGSLKDFHMSLSNITLLIVTIGATMLVLAV 584
 QY 601 TVTSLCIYLDLPWYLRMVCOMTQTRRRARNIPLBELQNLQPHAFISYSEHDSAMVKSGL 660
 DB 585 TVTSLCIYLDLPWYLRMVCOMTQTRRRARNIPLBELQNLQPHAFISYSEHDSAMVKSGL 644
 QY 661 VPYLEKEDIQICLHRNRPVSKSIYENIINCIEKSYKSIIFLSRPFQSEWCHLEYFAH 720
 DB 645 VPYLEKEDIQICLHRNRPVSKSIYENIINCIEKSYKSIIFLSRPFQSEWCHLEYFAH 704
 QY 721 HNLPHGSGNNILILILEPIPNKSKYHKLKALMTORTYQWPEKSKRGILFWANIRAA 780
 DB 705 HNLPHGSGNNILILILEPIPNKSKYHKLKALMTORTYQWPEKSKRGILFWANIRAA 764
 QY 781 FNMKLTLYTENNDVKS 796
 DB 765 FNMKLTLYTENNDVKS 780
 RESULT 10
 AAU25469
 ID AAU25469 standard; protein; 781 AA.
 AC AAU25469;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human mddt protein from clone LI:007302.1:2000MAY01.
 XX
 KW Human; molecules for disease detection and treatment; mddt;
 KW Antiarteriosclerotic; hepatotropic; antipapillary; cytosclerotic;
 KW immunosuppressive; antidiabetic; antiasclerotic; neuroprotective;
 KW osteopathic; antiautistic; cell proliferative disorder;
 KW arteriosclerosis; cirrhosis; psoriasis; cancer; adenocarcinoma;
 KW leukemia; breast cancer; autoimmune disorder; AIDS;
 KW acquired immunodeficiency syndrome; Addison's disease; diabetes mellitus;
 KW asthma; multiple sclerosis; osteoarthritis.
 KW
 OS Homo sapiens.
 PN WO200162922-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 21-FEB-2001; 2001WO-US005896.
 XX
 PR 24-FEB-2000; 2000US-0185213P.
 PR 16-MAY-2000; 2000US-0205232P.
 PR 17-MAY-2000; 2000US-0205285P.
 PR 17-MAY-2000; 2000US-0205286P.
 PR 17-MAY-2000; 2000US-0205287P.
 PR 17-MAY-2000; 2000US-0205323P.
 PR 17-MAY-2000; 2000US-0205324P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX

PI Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC,
PI Chen A, D'sa SA, Amshay S, Dahl CR, Dam TC, Daniels SE, Dufour GB,
PI Flores V, Fong WT, Greenwalt IB, Hillman JL, Jones AL, Liu TF,
PI Roseberry AM, Rosen BH, Russo FD, Stockbrecher TK, Daffo A,
PI Wright RJ, Yap PW, Yu JY, Bradley DL, Bratcher SR, Chen W,
PI Cohen HU, Hodgson DM, Lincoln SE, Jackson S;
DR WPI; 2001-570631/64.
DR N-PSDB; AAS42521.
XX
XX
XX New disease detection and treatment molecule polynucleotides and
PT polypeptides, useful for diagnosis and treatment of arteriosclerosis,
PT cirrhosis, psoriasis, cancer, autoimmune disorders, diabetes mellitus,
PT asthma and multiple sclerosis.
PS
PS Claim 27; Page 180-182; 183pp; English.
XX
XX The invention relates to novel human molecules for disease detection and
CC treatment (mdt proteins) and the polynucleotides encoding them. The MDT
CC polynucleotides and polypeptides are useful for diagnostic and
CC therapeutic purposes e.g. to diagnose and treat cell proliferative
CC disorders (e.g. arteriosclerosis, cirrhosis and psoriasis) cancers (e.g.
CC adenocarcinoma, leukemia and breast cancer) autoimmune disorders (e.g.
CC acquired immunodeficiency syndrome (AIDS) and Addison's disease) diabetes
CC mellitus, asthma, multiple sclerosis, osteoarthritis, and many more
CC diseases given in the specification. The present sequence represents an
CC mdt protein of the invention
XX
SQ Sequence 781 AA;
Query Match 96.8%; Score 4021; DB 4; Length 781;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTKDEPIVKSFFHFCVCLMIIIVGTRIOFSDGNEFAVDKSKRGLIHVPKDLPIKTVLDM 60
DB 7 MTKDEPIVKSFFHFCVCLMIIIVGTRIOFSDGNEFAVDKSKRGLIHVPKDLPIKTVLDM 66
QY 61 QNYIAELOVSDMSFISELTVLRSLSHNRIOQLDLSVFKFNODLEYDLSHNOLOKISCHPI 120
DB 67 QNYIAELOVSDMSFISELTVLRSLSHNRIOQLDLSVFKFNODLEYDLSHNOLOKISCHPI 126
QY 121 VSPRHLDSFNDKALPICKERFNGTNSQNLFLGLSAMKLOKDLPLPAHHLSTYILLDM 180
DB 127 VSPRHLDSFNDKALPICKERFNGTNSQNLFLGLSAMKLOKDLPLPAHHLSTYILLDM 186
QY 181 YYIKENETESLOILNAKTLHLVHFPTSLFAIQVNISVNTLGLQLOLTKANDNCQVFIK 240
DB 187 YYIKENETESLOILNAKTLHLVHFPTSLFAIQVNISVNTLGLQLOLTKANDNCQVFIK 246
QY 241 FLSELTIRSTLINFNLNIEETWKCLVRFQFLMKRPVEYINIVLTIESTREEDPTYS 300
DB 247 FLSELTIRSTLINFNLNIEETWKCLVRFQFLMKRPVEYINIVLTIESTREEDPTYS 306
QY 301 KTKLALTIETHTNOVFLFSOTALYTFSENMIMMLTISDPFIHMLCPHASTFKPLNF 360
DB 307 KTKLALTIETHTNOVFLFSOTALYTFSENMIMMLTISDPFIHMLCPHASTFKPLNF 366
QY 361 TQNVFTDSIFEKCSFLVLETLILQKNGKDLFKVGLMTKMPSEIILDVSNLSGSRH 420
DB 367 TQNVFTDSIFEKCSFLVLETLILQKNGKDLFKVGLMTKMPSEIILDVSNLSGSRH 426
QY 421 KENCWWSIIVLNLSSNMULTSVRCLPRTIKUTDHSNKLKSPKQVYKLEALQELNV 480
DB 427 KENCWWSIIVLNLSSNMULTSVRCLPRTIKUTDHSNKLKSPKQVYKLEALQELNV 486
QY 481 AFNSITJDPGCGSFSSLSVLIIDHNSVSHPSADFPQSCQKMSIKAGNDFPQCTELREF 540
DB 487 AFNSITJDPGCGSFSSLSVLIIDHNSVSHPSADFPQSCQKMSIKAGNDFPQCTELREF 546
QY 541 VKNIDQVSSEVLGMPDSYKCDYPSYRSGSPKDFHMSLSCNITLLITVITGATMLVLAV 600
DB 547 VKNIDQVSSEVLGMPDSYKCDYPSYRSGSPKDFHMSLSCNITLLITVITGATMLVLAV 606

QY 601 TYSICITVLDLPMYLRMVCQWOTRRRARNIPLEELQRLQPHAFISYSEHDSAMYSSEL 660
DB 607 TYSICITVLDLPMYLRMVCQWOTRRRARNIPLEELQRLQPHAFISYSEHDSAMYSSEL 666
QY 661 VPLEKEDIQICLHERNPVPGKSIYENIINCIEKSYKSIFFVLSPNFVQSEWCHELYEYFAH 720
DB 667 VPLEKEDIQICLHERNPVPGKSIYENIINCIEKSYKSIFFVLSPNFVQSEWCHELYEYFAH 726
QY 721 HNLFFHGSNNLLILLLEPIPNISIPKHKALKALMTORTYLOMPKSKRG 771
DB 727 HNLFFHGSNNLLILLLEPIPNISIPKHKALKALMTORTYLOMPKSKRG 777
RESULT 11
ADU23197
ID ADU23197 standard; protein; 795 AA.
XX
XX ADU23197;
AC
XX 27-JAN-2005 (first entry)
DT
XX Murine Toll-like receptor 6 (TLR6) protein - SEQ ID 89.
DE
XX screening; Toll-like receptor agonist; TLR agonist; TLR6.
KW
XX Mus sp.
OS
XX WO2004094671-A2.
PN
XX 04-NOV-2004.
PD
XX 22-APR-2004; 2004WO-US012788.
PF
XX 22-APR-2003; 2003US-0464586P.
PR
XX 22-APR-2003; 2003US-0464588P.
XX
PA (COLE-) COLEY PHARM GMBH.
PA (COLE-) COLEY PHARM GROUP INC.
PI
XX Volmer J, Jurek M, Lipford GB, Schetter C, Forebach A, Krieg AM,
DR WPI; 2004-795573/78.
XX
XX Identifying agonists of Toll-like receptor (TLR) signaling activity.
PT useful therapeutically or prophylactically, comprises contacting an
PT RPM18226 cell that expresses a TLR with a test compound and measuring TLR
PT signaling activity.
XX
XX Disclosure; SEQ ID NO 89; 342pp; English.
PS
XX The invention comprises a screening method for identifying agonists of
XX Toll-like receptor (TLR) signaling activity. The method involves
XX contacting an RPM18226 cell (that expresses a TLR) with a test compound,
XX and measuring a test level of TLR signaling activity, where a test level
XX that is positive is indicative of a test compound that is a TLR agonist.
XX The method of the invention is useful for identifying agonists of TLR.
XX The present amino acid sequence represents a TLR protein.
XX
SQ Sequence 795 AA;
Query Match 75.7%; Score 3144.5; DB 8; Length 795;
Best Local Similarity 73.9%; Pred. No. 3.9e-254;
Matches 588; Conservative 97; Mismatches 110; Indels 1; Gaps 1;
QY 1 MTKDEPIVKSFFHFCVCLMIIIVGTRIOFSDGNEFAVDKSKRGLIHVPKDLPIKTVLDM 60
DB 1 MSQDRKPIVGSFFHFCVCLMIIIVGTRIOFSDGNEFAVDKSKRGLIHVPKDLPIKTVLDM 60
QY 61 QNYIAELOVSDMSFISELTVLRSLSHNRIOQLDLSVFKFNODLEYDLSHNOLOKISCHPI 120
DB 61 QNYIAELOVSDMSFISELTVLRSLSHNRIOQLDLSVFKFNODLEYDLSHNOLOKISCHPI 120


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QY 121 VSPRLDLSFNDPFAKLPICKFEGNLSQNLFGLSAMKLOKLDLPIAHLSYLLDLRN 180
Db 121 ASLRLHDLSDFNDPVLVPCKEFGNLTUKLTPGLSLNAKFRQDLDPVAHLHLSCLLDLVS 180
QY 181 YYIKENETESIQIINAKTLHLVPHFTSLFAIQVNI SVNTTIGLOLTINIKANDNQVFIK 240
Db 181 YHIKGFETESIQIPNTTVLHLVPHFNLSLFSQVNNVSVALGHLQSLNKIDENDCQRLMT 240
QY 241 FLSLSTRGSTLLNFTLNHIETTWKCLVAVFOFLMPKPEYININYLITTESIREDEFTYS 300
Db 241 FLSLSTRGSTLLNFTLNHIETTWKCLVAVFOFLMPKPEYININYLITTESIREDEFTYS 300
QY 301 KTLTKALTIETHTNOVFLFSQALYTVFSENNIMMLTISDPFIHMLCPHAPSTFKPLNF 360
Db 301 ETALKSLMIEHVKNQVFLFSKALYSVFAEMNIKMLISDPFIHMLCPHAPSTFKPLNF 360
QY 361 TQNVFTDSIFPKCSTLVKLETLILQKNGIKDLFKVGLMTKMPSELIIDVSNLSGGRH 420
Db 361 TQNVFTDSVFOGCSLTKRLQTLILQKNGIKDLFKVGLMTKMPSELIIDVSNLSHAY 420
QY 421 KENCWVESIVVNLSSNMLTDSVFRCLPRLIKVLDLSNKKISVYKQVVKLEALQELNV 480
Db 421 DRTCAMASILVNLSSNMLTDSVFRCLPRLIKVLDLSNKKISVYKQVVKLEALQELNV 480
QY 481 AFNSLTLDIPGCGSFSSLSVLIIDHNSVSHPSADFPQSCQKMSIRAGDNPFQCTCELEEF 540
Db 481 ASNSLTLDIPGCGAFSSLSVLIIDHNSVSHPSADFPQSCQKMSIRAGDNPFQCTCELEEF 540
QY 541 VKNIDQVSSEVLGMPDSYKCDYPESYRGSPLKDRHMSPLSCNITLLITVITGATMLVLA 600
Db 541 VKNIGVAREVVEGMPDSYKCDYPESYRGSPLKDRHMSPLSCNITLLITVITGATMLVLA 600
QY 601 TVTSLCIYLDLPWYLRMVCWOTRRRARNIPLEELQRLQPHAFISYSEHDSAMVKSSEL 660
Db 601 TGAFLCIYFDLPWYLRMVCWOTRRRARNIPLEELQRLQPHAFISYSEHDSAMVKSSEL 660
QY 661 VPELEKEDIQICLHERNFVPGKSIYENINICIEKSYKSIYVLSPNFVQSEWCHYELYPAN 720
Db 661 LPNLEKEDIRVCLHERNFVPGKSIYENININIEKSKAIFVLSPHIQSEWCHYELYPAN 720
QY 721 HNLFHSGSNLILILIEPIPNISIPNKYHKLKALMTORTYLOWPKEKSKRGIFMANIRAF 780
Db 721 HNLFHSGSNLILILIEPIPNISIPNKYHKLKALMTORTYLOWPKEKSKRGIFMANIRAF 780
QY 781 FNMKLTIVTENNDDYKS 796
Db 781 FNMKLTIVTENNDDYKS 796
Db 781 FTMKLAIVNE-DDVKT 795

RESULT 12
ADU23195
ID ADU23195 standard; protein; 806 AA.
XX
AC ADU23195;
XX
XX 27-JAN-2005 (first entry)
XX
Db Murine Toll-like receptor 6 (TLR6) protein - SEQ ID 87.
XX
XX screening; Toll-like receptor agonist; TLR agonist; TLR6.
XX
OS Mus sp.
XX
XX WO2004094671-A2.
XX
PD 04-NOV-2004.
XX
PF 22-APR-2004; 2004MO-US012788.
XX
XX 22-APR-2003; 2003US-0464586P.
XX
PR 22-APR-2003; 2003US-0464588P.
XX
XX (COLE-) COLEY PHARM GMBH.

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PA (COLE-) COLEY PHARM GROUP INC.
XX
XX Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
XX WPI; 2004-795573/78.
DR
XX Identifying agonists of Toll-like receptor (TLR) signaling activity,
XX useful therapeutically or prophylactically, comprises contacting an
XX PT RPM18226 cell that expresses a TLR with a test compound and measuring TLR
XX signaling activity.
XX
PS Disclosure; SEQ ID NO 87; 342bp; English.
XX
XX The invention comprises a screening method for identifying agonists of
XX CC Toll-like receptor (TLR) signaling activity. The method involves
XX CC contacting an RPM18226 cell (that expresses a TLR) with a test compound,
XX CC and measuring a test level of TLR signalling activity, where a test level
XX CC that is positive is indicative of a test compound that is a TLR agonist.
XX CC The method of the invention is useful for identifying agonists of TLR.
XX CC The present amino acid sequence represents a TLR protein.
XX
SQ Sequence 806 AA;
Query Match 75.7%; Score 3144.5; DB 8; Length 806;
Best Local Similarity 72.9%; Pred. No. 4e-254;
Matches 588; Conservative 97; Mismatches 110; Indels 1; Gaps 1;
QY 1 MTKDKPEIVKSFHFVCLMIIIVGTRIQFSDNGEPAVDKSKRGLIHVPDLPKTKVLDMS 60
Db 12 MSQDRKPIVSFHVYCALALVSGMTFPSNLESMVYSNNNLHVHXPDPPTKALSLIS 71
QY 61 QNYIAELQVSDMSFLSELTVALRSLSHNRIOQLDLSVFKENODLELYDLSHNOLOKISCHPI 120
Db 72 QNSISELMPDISFLSELRVLRSLSHNRIRSDPFFVFLFNODLELYDLSHNRLOMISCCPM 131
QY 121 VSPRLDLSFNDPFAKLPICKFEGNLSQNLFGLSAMKLOKLDLPIAHLSYLLDLRN 180
Db 121 ASLRLHDLSDFNDPVLVPCKEFGNLTUKLTPGLSLNAKFRQDLDPVAHLHLSCLLDLVS 191
QY 181 YYIKENETESIQIINAKTLHLVPHFTSLFAIQVNI SVNTTIGLOLTINIKANDNQVFIK 240
Db 181 YHIKGFETESIQIPNTTVLHLVPHFNLSLFSQVNNVSVALGHLQSLNKIDENDCQRLMT 251
QY 241 FLSLSTRGSTLLNFTLNHIETTWKCLVAVFOFLMPKPEYININYLITTESIREDEFTYS 300
Db 241 FLSLSTRGSTLLNFTLNHIETTWKCLVAVFOFLMPKPEYININYLITTESIREDEFTYS 311
QY 301 KTLTKALTIETHTNOVFLFSQALYTVFSENNIMMLTISDPFIHMLCPHAPSTFKPLNF 360
Db 301 ETALKSLMIEHVKNQVFLFSKALYSVFAEMNIKMLISDPFIHMLCPHAPSTFKPLNF 371
QY 361 TQNVFTDSIFPKCSTLVKLETLILQKNGIKDLFKVGLMTKMPSELIIDVSNLSGGRH 420
Db 361 TQNVFTDSVFOGCSLTKRLQTLILQKNGIKDLFKVGLMTKMPSELIIDVSNLSHAY 431
QY 421 KENCWVESIVVNLSSNMLTDSVFRCLPRLIKVLDLSNKKISVYKQVVKLEALQELNV 480
Db 421 DRTCAMASILVNLSSNMLTDSVFRCLPRLIKVLDLSNKKISVYKQVVKLEALQELNV 491
QY 481 AFNSLTLDIPGCGSFSSLSVLIIDHNSVSHPSADFPQSCQKMSIRAGDNPFQCTCELEEF 540
Db 481 ASNSLTLDIPGCGAFSSLSVLIIDHNSVSHPSADFPQSCQKMSIRAGDNPFQCTCELEEF 551
QY 541 VKNIDQVSSEVLGMPDSYKCDYPESYRGSPLKDRHMSPLSCNITLLITVITGATMLVLA 600
Db 541 VKNIGVAREVVEGMPDSYKCDYPESYRGSPLKDRHMSPLSCNITLLITVITGATMLVLA 611
QY 601 TVTSLCIYLDLPWYLRMVCWOTRRRARNIPLEELQRLQPHAFISYSEHDSAMVKSSEL 660
Db 601 TGAFLCIYFDLPWYLRMVCWOTRRRARNIPLEELQRLQPHAFISYSEHDSAMVKSSEL 671
QY 661 VPELEKEDIQICLHERNFVPGKSIYENINICIEKSYKSIYVLSPNFVQSEWCHYELYPAN 720
Db 661 VPELEKEDIQICLHERNFVPGKSIYENININIEKSKAIFVLSPHIQSEWCHYELYPAN 720

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Db      672 LPLEKDDIRVCLHBRNFPVPGKSIIVENIINFEKSYKAIPLVLSPHFIOSEWCHYEYFAH 731
Qy      721 HNLPHGSGNNLILILEPIPNISIPNKYHKLKALMTORTYLOMPKESKRGLFMANIRAA 780
Db      732 HNLPHGSGNNLILILEPIPNISIPNKYHKLKALMTORTYLOMPKESKRGLFMANIRAS 791
Qy      781 FNMKLTLYTENNDVKS 796
Db      792 FIMKIALVNE-DVKT 806

RESULT 13
ID      AAY8055
XX      AAY8055 standard; protein; 806 AA.
AC      AAY8055;
XX      DT
XX      22-SEP-2000 (first entry)
XX      DE
XX      Murine Toll-like receptor TLR6 protein.
XX      KM
XX      Toll-like receptor; TLR6; murine; anti-infectious; treatment; infection;
XX      KM
XX      transcription factor; NF-kappaB; immune response.
XX      OS
XX      Mus sp.
XX      PN
XX      WO200024776-A1.
XX      PD
XX      04-MAY-2000.
XX      PF
XX      26-OCT-1999; 99WO-JP005917.
XX      PR
XX      26-OCT-1998; 98JP-00304110.
XX      PA
XX      (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX      PI
XX      Akira S, Takeuchi O;
XX      DR
XX      WPI; 2000-350697/30.
XX      DR
XX      N-PSDB; AAA39810.
XX      PT
XX      Toll-like receptor TLR6 molecule and encoded gene, participating in
XX      PT
XX      signal transduction of initial immune response, applicable e.g. in
XX      PT
XX      treating infections.
XX      PS
XX      Claim 1; Page 31-33; 35pp; Japanese.
XX      CC
XX      This invention describes a novel toll-like receptor TLR6 which has
XX      CC
XX      anti-infectious activity. The protein and its encoded gene have clinical
XX      CC
XX      use e.g. in treating infections. Toll family receptors are related to
XX      CC
XX      transcription factor NF-kappaB and regulate the expression of various
XX      CC
XX      genes participating in the immune response. This sequence represents the
XX      CC
XX      murine TLR6 protein which is described in the method of the invention
XX      CC
XX      SQ
XX      Sequence 806 AA;

Query Match      75.6%; Score 3139.5; DB 3; Length 806;
Best Local Similarity 73.7%; Pred. No. 1e-253;
Matches 587; Conservative 98; Mismatches 110; Indels 1; Gaps 1;

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Db      192 HHKGGFESLQIPNTVTLHLVFNHNSLFSVQVNNSVNALGHLQSNIKLNDENCQRLMT 251
Qy      241 FLSLETRGSLTNFLNHIETTKCLVRFQGLMKPKVEYINLYNLTIIESTREDFYTS 300
Db      252 FLSLETRGSLTNFLNHIETTKCLVRFQGLMKPKVEYINLYNLTIIESTREDFYTS 311
Qy      301 KTLKALTTEHTNQVFLPSOTALTVESENNIMMLTISDPFIHMLCPHASTKFLNF 360
Db      312 ETALKSLMEIHKVNOVFLFSKALYSVFAENNIKNLSISDTPIHMCDFPSSSTFLNF 371
Qy      361 TONVEFDSIFEKCSITVVKLETLILQKNGIKDLFKVGLMTKMPSEIILDVSNMSLESGRH 420
Db      372 TONVEFDSIFQGCSTLTKRLQTLILQKNGIKNFVKALMTKNNSSLETIDVLSNLSNAY 431
Qy      421 KENCTWESIVVNLNLSNMLTDSVRCCLPRIKVLDHSNKTKSVPKOVYKLEALQELNV 480
Db      432 DRTCAMAESITVLNLSNMLTGSVRCCLPRIKVLDHSNKTKSVPKOVYKLEALQELNV 491
Qy      481 AFNSLITDLPGCGSFSLSVLIIIDHNSVSHPSADFQSCQKRSIKAGDNPCCTELREF 540
Db      492 ASNSLITDLPGCGSFSLSVLVIDHNSVSHPSDFQSCQKRSIKAGDNPCCTELREF 551
Qy      541 VKNIDQVSEVLEGPDSYKCDPESYRGSPLKDFHMSLSNITLITVIGATMLVLAV 600
Db      552 VKNIGVAREVVEGPDSDYKCDPESYRGSPLKDFHMSLSNITLITVIGATMLVLAV 611
Qy      601 TVTSLCTIYLDLPYIRAVCOMTQTRRARNIPLEELQNLQPHAFISYSEHDSAVKSEL 660
Db      612 TGAFLCTLYFDLPWYVYRMLCQWOTQTRRARNIPLEELQNLQPHAFISYSEHDSAVKSEL 671
Qy      661 VPLEKEDIOICLHERNFVPGKSIIVENIINFEKSYKAIPLVLSPHFIOSEWCHYEYFAH 720
Db      672 LPLEKDDIRVCLHBRNFPVPGKSIIVENIINFEKSYKAIPLVLSPHFIOSEWCHYEYFAH 731
Qy      721 HNLPHGSGNNLILILEPIPNISIPNKYHKLKALMTORTYLOMPKESKRGLFMANIRAA 780
Db      732 HNLPHGSGNNLILILEPIPNISIPNKYHKLKALMTORTYLOMPKESKRGLFMANIRAS 791
Qy      781 FNMKLTLYTENNDVKS 796
Db      792 FIMKIALVNE-DVKT 806

RESULT 14
ID      ADU23194
XX      ADU23194 standard; protein; 806 AA.
XX      AC
XX      ADU23194;
XX      DT
XX      27-JAN-2005 (first entry)
XX      DE
XX      Murine Toll-like receptor 6 (TLR6) protein - SEQ ID 86.
XX      KM
XX      screening; Toll-like receptor agonist; TLR agonist; TLR6.
XX      OS
XX      Mus sp.
XX      PN
XX      WO2004094671-A2.
XX      PD
XX      04-NOV-2004.
XX      PF
XX      22-APR-2004; 2004WO-US012788.
XX      PR
XX      22-APR-2003; 2003US-0464586P.
XX      PR
XX      22-APR-2003; 2003US-0464586P.
XX      PA
XX      (COLE-) COLEY PHARM GROUP INC.
XX      PI
XX      (COLE-) COLEY PHARM GROUP INC.
XX      DR
XX      Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
XX      WPI; 2004-795573/78.

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OM nucleic - nucleic search, using sw model

Run on: June 4, 2006, 23:11:41 ; Search time 1680 Seconds
(without alignments)
11425.357 Million cell updates/sec

Title: US-10-732-796A-11

Perfect score: 2753

Sequence: 1 agaattgcacatcatca.....ttcccaatgacatctctg 2753

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq.8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001s:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2753	100.0	2753	12	ADP56659 Human Tol
2	2753	100.0	2753	12	ADP48600 Human Tol
3	2753	100.0	2753	13	ADU23187 Human Tol
4	2753	100.0	2753	14	ADU23187 Human Tol
5	2748.8	99.8	2760	6	AAAD26300 Human DNA
6	2748.8	99.8	2760	13	ADU23186 Human Tol
7	2747.2	99.8	2760	3	AAA39809 Human Tol
8	2727.8	99.1	2940	5	AAA42521 Human Tol
9	2391	86.9	2391	14	AA42521 Human CDN
10	1533.6	55.7	2604	3	AAA39810 Human psy
11	1533.6	55.7	2604	13	ADU23191 Murine To
12	1533.6	55.7	2604	13	ADU23192 Murine To
13	1531.2	55.6	2421	13	ADU23193 Murine To
14	1445	52.5	2381	10	ADU23193 Murine To
15	1444.2	52.5	2358	10	ADU23193 Murine To
16	1444.2	52.5	2361	14	ADU23193 Murine To
17	1444.2	52.5	2367	2	AAV80663 Human DNA
18	1444.2	52.5	2367	6	AAAD26280 Human DNA

19	1444.2	52.5	2621	6	ABL65802	ABL65802 lung canc
20	1444.2	52.5	2832	12	ADP56659	ADP56659 Human Tol
21	1444.2	52.5	2832	12	ADP48590	ADP48590 Human Tol
22	1444.2	52.5	2832	13	ADP54895	ADP54895 Human PRO
23	1439.4	52.3	2806	6	ABK83579	ABK83579 Human CDN
24	1439.4	52.3	2806	10	ADBE25537	ADBE25537 Human TLR
25	1434.8	52.1	2831	10	ADBA7471	ADBA7471 Human CDN
26	777.2	28.2	3046	6	ADAD26299	ADAD26299 Human DNA
27	777.2	28.2	3462	2	AAK58297	AAK58297 Human Tol
28	777.2	28.2	3462	3	AA64960	AA64960 Membrane-
29	777.2	28.2	3462	4	AA646131	AA646131 Human DNA
30	777.2	28.2	3462	5	AA44106	AA44106 Human PRO
31	777.2	28.2	3462	8	ACA89581	ACA89581 CDNA enco
32	777.2	28.2	3462	8	ACA73591	ACA73591 Human sec
33	777.2	28.2	3462	8	ACA03906	ACA03906 Human sec
34	777.2	28.2	3462	8	ACA66740	ACA66740 Human sec
35	777.2	28.2	3462	8	ACA64193	ACA64193 CDNA enco
36	777.2	28.2	3462	8	ACF20315	ACF20315 Novel hum
37	777.2	28.2	3462	8	ACF19701	ACF19701 Human sec
38	777.2	28.2	3462	8	ACD21989	ACD21989 Human sec
39	777.2	28.2	3462	8	ACF13154	ACF13154 Human sec
40	777.2	28.2	3462	8	ACD25257	ACD25257 Human sec
41	777.2	28.2	3462	8	ACF00306	ACF00306 Human sec
42	777.2	28.2	3462	8	ACA72363	ACA72363 Novel hum
43	777.2	28.2	3462	8	ACD04887	ACD04887 Human sec
44	777.2	28.2	3462	8	ACD18348	ACD18348 Human sec
45	777.2	28.2	3462	8	ACD08355	ACD08355 Human sec

ALIGNMENTS

RESULT 1	
ADP56659	standard; DNA; 2753 BP.
ID	ADP56659
XX	
AC	ADP56659;
XX	
DT	09-SEP-2004 (first entry)
XX	
DE	Human Toll-like receptor TLR6 DNA - SEQ ID 11.
XX	
KW	expression system; Toll-like receptor; TLR6; immune response modifier;
KW	IRN; cancer; gene therapy; human; ds; gene.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	/*tag= a
FT	/product= "Human Toll-like receptor TLR6 protein - SEQ ID 12"
XX	
PN	W02004053057-A2.
XX	
PD	24-JUN-2004.
XX	
PF	31-OCT-2003; 2003WO-US034563.
XX	
PR	11-DEC-2002; 2002US-0432651P.
XX	
PA	(MINTN) 3M INNOVATIVE PROPERTIES CO.
XX	
PI	Gupta SK, Ghosh TK, Fink JR;
XX	
DR	WPI; 2004-468833/44.
XX	
DR	P-PSDB; ADP56660.
XX	
PT	New expression system comprising a first nucleic acid sequence that
PT	encodes a Toll-like receptor (TLR), useful for preparing a composition
PT	comprising TLR agonist for treating e.g., cancer.
XX	
PS	Claim 3; SEQ ID NO 11; 69pp; English.

XX The invention relates to a novel expression system comprising a first
CC nucleic acid sequence that encodes a Toll-like receptor (TLR) operably
CC linked to a first expression control sequence and a second nucleic acid
CC sequence that encodes a reporter. TLRs are immune response modifiers
CC (IRMs). The expression system of the invention may be useful for
CC preparing a composition comprising the TLR agonist for treating cancer,
CC possibly via gene therapy. The current sequence is that of the human Toll
CC -like receptor TLR6 DNA (SEQ ID 11) of the invention.
XX

Sequence 2753 BP; 849 A; 559 C; 507 G; 838 T; 0 U; 0 Other;

Query Match 100.0%; Score 2753; DB 12; Length 2753;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 AGAATTGGACCTCATATCAAGATGCTCTGAGAGAGAAACAACCTTAGATGCCACATGC 60
Db 1 AGAATTGGACCTCATATCAAGATGCTCTGAGAGAGAAACAACCTTAGATGCCACATGC 60
OY 61 AACATCATGACCAAGACAAAGAACCTATTGTTAAAGCTTCCATTGTTGGCCTTAAG 120
Db 61 AACATCATGACCAAGACAAAGAACCTATTGTTAAAGCTTCCATTGTTGGCCTTAAG 120
OY 61 AACATCATGACCAAGACAAAGAACCTATTGTTAAAGCTTCCATTGTTGGCCTTAAG 120
Db 61 AACATCATGACCAAGACAAAGAACCTATTGTTAAAGCTTCCATTGTTGGCCTTAAG 120
OY 121 ATCATTAATAGTTGGAACCAAGATCCAGATCTCCGACGGAATGAATTGGCAGTAGACAAG 180
Db 121 ATCATTAATAGTTGGAACCAAGATCCAGATCTCCGACGGAATGAATTGGCAGTAGACAAG 180
OY 181 TCAAAAAGAGCTTATTCATCTTCCAAAAGACCTACCGCTGAAAAACCAAACTCTTAAGT 240
Db 181 TCAAAAAGAGCTTATTCATCTTCCAAAAGACCTACCGCTGAAAAACCAAACTCTTAAGT 240
OY 241 ATGTCTCAGAACTACATCGCTGAGCTTCAGGCTCTCTGACATGAGCTTTCTACAGATGG 300
Db 241 ATGTCTCAGAACTACATCGCTGAGCTTCAGGCTCTCTGACATGAGCTTTCTACAGATGG 300
OY 241 ATGTCTCAGAACTACATCGCTGAGCTTCAGGCTCTCTGACATGAGCTTTCTACAGATGG 300
Db 241 ATGTCTCAGAACTACATCGCTGAGCTTCAGGCTCTCTGACATGAGCTTTCTACAGATGG 300
OY 301 ACAGTTTTGAGACTTTCCCAATACAGAACTCAGCTACTGATTAAAGTCTTCAAGTTC 360
Db 301 ACAGTTTTGAGACTTTCCCAATACAGAACTCAGCTACTGATTAAAGTCTTCAAGTTC 360
OY 361 AACCGGATTTTGAATATTTTGAATTTATCTCATTAATCACTTGGCAAAAGATATCTCGCAT 420
Db 361 AACCGGATTTTGAATATTTTGAATTTATCTCATTAATCACTTGGCAAAAGATATCTCGCAT 420
OY 361 AACCGGATTTTGAATATTTTGAATTTATCTCATTAATCACTTGGCAAAAGATATCTCGCAT 420
Db 361 AACCGGATTTTGAATATTTTGAATTTATCTCATTAATCACTTGGCAAAAGATATCTCGCAT 420
OY 421 CCTATTGTGAGTTTCAAGCAATTTAATCTCTCATTCATGATTTTCAAGGCCCTGCCCATC 480
Db 421 CCTATTGTGAGTTTCAAGCAATTTAATCTCTCATTCATGATTTTCAAGGCCCTGCCCATC 480
OY 481 TGTAAAGAAATTTGGCACTTATCACAACCTGAATTTCTTGGGAATGAGTGTATGAAGCTG 540
Db 481 TGTAAAGAAATTTGGCACTTATCACAACCTGAATTTCTTGGGAATGAGTGTATGAAGCTG 540
OY 541 CAAAAATTAAGATTTGCTGCAATTTGCTCACTTGCATCTAAGTTAATCTCTTGGATTTTA 600
Db 541 CAAAAATTAAGATTTGCTGCAATTTGCTCACTTGCATCTAAGTTAATCTCTTGGATTTTA 600
OY 601 AGAAATTTATATATATAAAGAAATGAGACAGAAAGCTCTACAAATTTCTGATGCAAAAACC 660
Db 601 AGAAATTTATATATATAAAGAAATGAGACAGAAAGCTCTACAAATTTCTGATGCAAAAACC 660
OY 661 CTTCACCTTGTGTTTTCACCCAACTAAGTTATTGCTATCCAAAGTGAACATATCAGTTAAT 720
Db 661 CTTCACCTTGTGTTTTCACCCAACTAAGTTATTGCTATCCAAAGTGAACATATCAGTTAAT 720
OY 721 ACTTTAGGGTGTCTTACAACTGACTAATATTAATGAATGAGACAACAGTCAAGTTTTC 780
Db 721 ACTTTAGGGTGTCTTACAACTGACTAATATTAATGAATGAGACAACAGTCAAGTTTTC 780
OY 781 ATTTAATTTTATATCAGAACTCAGACAGAGGTTCAACCTTACGTAATTTTCAACCTCAACAC 840
Db 781 ATTTAATTTTATATCAGAACTCAGACAGAGGTTCAACCTTACGTAATTTTCAACCTCAACAC 840
OY 841 ATGAAACGACCTTGGAAATGCTGTGTCAGAGTCTTTCAATTTCTTTGGCCAAACCTGTG 900
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Db 841 ATGAAACGACCTTGGAAATGCTGTGTCAGAGTCTTTCAATTTCTTTGGCCAAACCTGTG 900
OY 901 GAATATCTCAATATTTTACAAATTTTAAACATATTTGAAACATCTTGGAGAGATTTTACT 960
Db 901 GAATATCTCAATATTTTACAAATTTTAAACATATTTGAAACATCTTGGAGAGATTTTACT 960
OY 961 TATTTTAAACGACATTTGAAAGCATTTGACAAATGAAATCATATCAGAACCAAGTTTTCG 1020
Db 961 TATTTTAAACGACATTTGAAAGCATTTGACAAATGAAATCATATCAGAACCAAGTTTTCG 1020
OY 1021 TTTTACAGACAGCTTTGTACACCGTGTGTTTCTGAGATGAACATTAATGATGTAACCAT 1080
Db 1021 TTTTACAGACAGCTTTGTACACCGTGTGTTTCTGAGATGAACATTAATGATGTAACCAT 1080
OY 1081 TCAGATACACCTTTTATACATGCTGTGTCTCTCATGACCAAGACATCAAGTTTTCG 1140
Db 1081 TCAGATACACCTTTTATACATGCTGTGTCTCTCATGACCAAGACATCAAGTTTTCG 1140
OY 1141 AACTTTACCCAGAAAGTTTTCACAGATAGTATTTTGAAGAAATGTTCCACGTTAGTTAAA 1200
Db 1141 AACTTTACCCAGAAAGTTTTCACAGATAGTATTTTGAAGAAATGTTCCACGTTAGTTAAA 1200
OY 1201 TTGAGACACTTATCTTCAAAAAATGATTAAGACCTTTTCAAGTAGTCTCATG 1260
Db 1201 TTGAGACACTTATCTTCAAAAAATGATTAAGACCTTTTCAAGTAGTCTCATG 1260
OY 1261 ACGAAGATATGCTCTTTGGAATACTGATGTAGCTGGAATCTTTGGAATCTGCT 1320
Db 1261 ACGAAGATATGCTCTTTGGAATACTGATGTAGCTGGAATCTTTGGAATCTGCT 1320
OY 1321 AGACATTAAGAAACCTGACCTTGGTGAAGATAGTGTGTTAAATTTGTCTTCAAT 1380
Db 1321 AGACATTAAGAAACCTGACCTTGGTGAAGATAGTGTGTTAAATTTGTCTTCAAT 1380
OY 1381 ATGCTTACTGACTCTGTTTTCAGATGTTTACCCTCCAGATCAAGTACTTGAAC 1440
Db 1381 ATGCTTACTGACTCTGTTTTCAGATGTTTACCCTCCAGATCAAGTACTTGAAC 1440
OY 1441 AGCAATTAATAAAGAGGCTCTCTTAAACAAGTGTAAATCTGAAAGCTTTGCAAGAACTC 1500
Db 1441 AGCAATTAATAAAGAGGCTCTCTTAAACAAGTGTGTAAATCTGAAAGCTTTGCAAGAACTC 1500
OY 1501 AATGTGCTTCAATTTCTTAACTGACCTTCTGAGTGTGCAAGCTTTTGAACGCTTTCT 1560
Db 1501 AATGTGCTTCAATTTCTTAACTGACCTTCTGAGTGTGCAAGCTTTTGAACGCTTTCT 1560
OY 1561 GTATTGATCATTTGATCACAATTTCAAGTTTCCCAACCAATGCGTGAATTTCTTCCAGAGCTGC 1620
Db 1561 GTATTGATCATTTGATCACAATTTCAAGTTTCCCAACCAATGCGTGAATTTCTTCCAGAGCTGC 1620
OY 1621 CAGAGATGAGGTCATTAAGCAAGGAGCAATCCATTCATGTAATGCTGTAGAGTAAGA 1680
Db 1621 CAGAGATGAGGTCATTAAGCAAGGAGCAATCCATTCATGTAATGCTGTAGAGTAAGA 1680
OY 1681 GAATTTGTCAAAAATATAGACCAAGTATCAAGTAAGTATAGAGGCTGTGCTGATTTCT 1740
Db 1681 GAATTTGTCAAAAATATAGACCAAGTATCAAGTAAGTATAGAGGCTGTGCTGATTTCT 1740
OY 1741 TATTAAGTGTGACTACCCGAAAGATTAAGAGAAAGCCCATTAAGAGACTTTTCAATGTCT 1800
Db 1741 TATTAAGTGTGACTACCCGAAAGATTAAGAGAAAGCCCATTAAGAGACTTTTCAATGTCT 1800
OY 1801 GAAATATCTGCAACATTAATCTGTGTATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1860
Db 1801 GAAATATCTGCAACATTAATCTGTGTATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1860
OY 1861 GCTGTGACTGTGACCTTCCCTCTGCACTTACTGTGATCTGCTGTGATCTGAGATGATG 1920
Db 1861 GCTGTGACTGTGACCTTCCCTCTGCACTTACTGTGATCTGCTGTGATCTGAGATGATG 1920
OY 1921 TGCAGTGGACCCAGACTCTGGGCGAGGGCCAGGAACATACCTTTGAAGAACTCCAAAGA 1980
Db 1921 TGCAGTGGACCCAGACTCTGGGCGAGGGCCAGGAACATACCTTTGAAGAACTCCAAAGA 1980
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Db 1921 TGCCAGTGAGCCAGACTGCGGCGAGGCGCAGAAACATACCTTAGAAGAACTCCAAAGA 1980
Qy 1981 AACCTCAGATTTCATGCTTTTATTTATTTAGTAAGAACATATTCGCGGAGGAAAGT 2040
Db 1981 AACCTCAGATTTCATGCTTTTATTTATTTAGTAAGAACATATTCGCGGAGGAAAGT 2040
Qy 2041 GAATTGGTACCTTACCTTAGAAGAAAGATATATACAGATTGCTTCATGAGAGAACTTT 2100
Db 2041 GAATTGGTACCTTACCTTAGAAGAAAGATATATACAGATTGCTTCATGAGAGAACTTT 2100
Qy 2101 GTCCCTGGCAAGAGCATTTGTGAAATATATCATCACTGATGAGAGAGTTACAAAGTCC 2160
Db 2101 GTCCCTGGCAAGAGCATTTGTGAAATATATCATCACTGATGAGAGAGTTACAAAGTCC 2160
Qy 2161 ATCTTGTGTTTGTCCCAACTTGTCCAGAGTGTGTGCTTATGCAACTATTTT 2220
Db 2161 ATCTTGTGTTTGTCCCAACTTGTCCAGAGTGTGTGCTTATGCAACTATTTT 2220
Qy 2221 GCCCATCACAATCTCTTTCATGAGAGATCTAATTAATCTTCATCTTACGAAACC 2280
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Qy 2281 ATTCACAGAGAGAGATTCACCAAGTACCAAGCTGAGAGCTCTCATGACGACGCG 2340
Db 2281 ATTCACAGAGAGAGATTCACCAAGTACCAAGCTGAGAGCTCTCATGACGACGCG 2340
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Db 2341 ACTTATTTGCACTGGCCCAAGAGAAAGCAACGCGGCTCTTTTGGGCTTAACATTAGA 2400
Qy 2401 GCCGCTTTTATATGAAATTAACACTAGTCACTGAAAAAATGATGTAATCTTAAAAA 2460
Db 2401 GCCGCTTTTATATGAAATTAACACTAGTCACTGAAAAAATGATGTAATCTTAAAAA 2460
Qy 2461 AATTAGGAATTAACCTTAAGAAACCATTAATTAATCTTGATGATGATGATGATGATGAT 2520
Db 2461 AATTAGGAATTAACCTTAAGAAACCATTAATTAATCTTGATGATGATGATGATGATGAT 2520
Qy 2521 CGTAGTAATCTGTCGAGAGTCCCTCCATTAATCCATGATGATGATGATGATGATGATGAT 2580
Db 2521 CGTAGTAATCTGTCGAGAGTCCCTCCATTAATCCATGATGATGATGATGATGATGATGAT 2580
Qy 2581 AAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
Db 2581 AAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
Qy 2641 AGCCAGTCTCTTCTGTTTATCATTAATGTTTCAAAATGAAACAGTCTCTTTGATGA 2700
Db 2641 AGCCAGTCTCTTCTGTTTATCATTAATGTTTCAAAATGAAACAGTCTCTTTGATGA 2700
Qy 2701 ATGCTCAGTTTTCAGTCTCTTCTCCTGCTTCCCACTGCTTCCCAATGATGATGATG 2753
Db 2701 ATGCTCAGTTTTCAGTCTCTTCTCCTGCTTCCCACTGCTTCCCAATGATGATGATG 2753

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RESULT 2
ADP48600
ID ADP48600 standard; cDNA, 2753 BP.
XX
XX ADP48600;
XX
XX 09-SEP-2004 (first entry)
XX
XX Human Toll-like receptor 6 encoding cDNA SEQ ID NO:11.
XX
XX Toll-like receptor; TLR; human; detection; identification; TLR agonist;
XX TLR antagonist; Toll like receptor 6; TLR6; chromosome 4; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 67..2457
XX FT /*tag= a

```

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FT /product= "Toll-like receptor 6"
XX
XX MO2004053452-A2.
XX
XX 24-JUN-2004.
XX
XX 31-OCT-2003; 2003WO-US034554.
XX
XX 11-DEC-2002; 2002US-0432650P.
XX
XX (MINN) 3M INNOVATIVE PROPERTIES CO.
XX
XX Gupta SK, Ghosh TK, Fink JR;
XX
XX WPI: 2004-468955/44.
XX P-FSDB; ADP48601.
XX DR GENBANK; NM_006068.
XX
XX Detecting activation of Toll-like receptors (TLR) for identifying a TLR
XX agonist or antagonist, comprises providing a cell culture comprising
XX cells transfected with a sequence encoding a reporter.
XX
XX Claim 7; SEQ ID NO 11; 78bp; English.
XX
XX The present invention describes a method for detecting activation of a
XX Toll-like receptor (TLR) in a cell. The method comprises: (a) providing a
XX cell culture comprising cells transfected with a nucleic acid sequence
XX that encodes a reporter that (1) generates a detectable signal when the
XX reporter is expressed and the cell is exposed to conditions for
XX generating the detectable signal, and (ii) is operably linked to an
XX expression control sequence that is induced by activation of a TLR and
XX comprises a cytokine promoter, a chemokine promoter, a co-stimulatory
XX marker promoter, or a defensin promoter; (b) exposing the cell culture to
XX a compound that activates a TLR; (c) providing conditions for generating
XX the detectable signal; and (d) detecting the detectable signal. Also
XX described: (1) a method of identifying a TLR agonist or antagonist; (2) a
XX TLR agonist or antagonist identified by the method of (1); and (3) a
XX pharmaceutical composition comprising a TLR agonist or antagonist
XX identified by the method of (1) and a pharmaceutical salt. The methods
XX are useful for detecting activation of a TLR in a cell and for
XX identifying TLR agonist or antagonist. The present sequence encodes a
XX human TLR6 which is used in the exemplification of the present invention.
XX The human TLR6 gene is located on chromosome 4, more specifically to
XX 4p14.
XX
XX Sequence 2753 BP; 849 A; 559 C; 507 G; 838 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 2753; DB 12; Length 2753;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AGAATTTGGACTCATATCAAGATGCTCTGAGAGAGAACAAACCTTTAGAGATGACACTGC 60
XX 1 AGAATTTGGACTCATATCAAGATGCTCTGAGAGAGAACAAACCTTTAGAGATGACACTGC 60
XX
XX 61 AACATCATGACCAAGAACAAAGAACTTATTTGTTAAAGCTTTCATTTTGTGCTTATG 120
XX 61 AACATCATGACCAAGAACAAAGAACTTATTTGTTAAAGCTTTCATTTTGTGCTTATG 120
XX
XX 121 ATCATTAATAGTTGGAACCAAGAACTTCTCCAGCGGAAATGAATTTGAGTAGACAAAG 180
XX 121 ATCATTAATAGTTGGAACCAAGAACTTCTCCAGCGGAAATGAATTTGAGTAGACAAAG 180
XX
XX 181 TCAAAAAGAGGCTTATTCATGTTTCCAAAAGACTTACCGCTGAAAACCAAGTCTTAAT 240
XX 181 TCAAAAAGAGGCTTATTCATGTTTCCAAAAGACTTACCGCTGAAAACCAAGTCTTAAT 240
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XX 241 ATGCTCAGAACTACATGCTGAGCTTCAAGGCTCTGACATGATGAGCTTCTATCAAGTTG 300
XX 241 ATGCTCAGAACTACATGCTGAGCTTCAAGGCTCTGACATGATGAGCTTCTATCAAGTTG 300
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XX 301 ACAGTTTGAAGCTTCCCATTAACGAATCCAGCTACTTGAATTAAGTGTGTTTCAAGTTG 360

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Db 301 ACAGTTTGAGACTTTCCCAATACAGAACTCAGCTACTGATTTAAGTGTTCATGATTC 360
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Db 361 AACCGAGATTGAAATATTTGGATTATCTCATTAATCAGTTGCGAAAGATATCTGCCAT 420
Qy 421 CCTATGTGAGTTTCAGGCATTTAAGTCTCTCATTCATGATGATTTCAAGGCCCTGCCATC 480
Db 421 CCTATGTGAGTTTCAGGCATTTAAGTCTCTCATTCATGATGATTTCAAGGCCCTGCCATC 480
Qy 481 TGTAGGAATTTGGCACTTATCACACTGAAATTTCTGGGATGAGTGTGCTATGAAAGCTG 540
Db 481 TGTAGGAATTTGGCACTTATCACACTGAAATTTCTGGGATGAGTGTGCTATGAAAGCTG 540
Qy 541 CAAAAATTAGATTGCTGCGCAATTCCTCACTTGCACTTAAGTTAATCTCTTGAGATTTA 600
Db 541 CAAAAATTAGATTGCTGCGCAATTCCTCACTTGCACTTAAGTTAATCTCTTGAGATTTA 600
Qy 601 AGAAATTTATATATAAAGAAAATGAGACAGAAAGTCTACAAATTTCTGAATGCCAAAAC 660
Db 601 AGAAATTTATATATAAAGAAAATGAGACAGAAAGTCTACAAATTTCTGAATGCCAAAAC 660
Qy 661 CTTCACCTGTTTTTCAACCACTGATTTATTCGCTATTCGAAGTGAACATCAGTTAT 720
Db 661 CTTCACCTGTTTTTCAACCACTGATTTATTCGCTATTCGAAGTGAACATCAGTTAT 720
Qy 721 ACTTAAAGGTCCTTACAACTGACTATATATTAATTTGAATGATGACAACTGTCAGATTTC 780
Db 721 ACTTAAAGGTCCTTACAACTGACTATATATTAATTTGAATGATGACAACTGTCAGATTTC 780
Qy 781 ATTAATTTTATATCGAACTACAGAGGTTCAACCTTATCTGAATTTTACCTCAACAC 840
Db 781 ATTAATTTTATATCGAACTACAGAGGTTCAACCTTATCTGAATTTTACCTCAACAC 840
Qy 841 ATAGAAGAGCTTGGAAATGCGTGTGACAGTCTTCAATTTCTTTGGCCCAACCTG 900
Db 841 ATAGAAGAGCTTGGAAATGCGTGTGACAGTCTTCAATTTCTTTGGCCCAACCTG 900
Qy 901 GAATATCTCAATATTTACATTTAAACAATAATTTGAAAGCATTCGTGAGAAAGATTACT 960
Db 901 GAATATCTCAATATTTACATTTAAACAATAATTTGAAAGCATTCGTGAGAAAGATTACT 960
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Db 961 TATTTTAAAGCAGCATTTGAAAGCATTTGACAAATGAAACATATCAGAACCAAGTTTCTG 1020
Qy 1021 TTTTACAGAGAGCTTTGACACCGTGTCTTCTGAGATGAGACATTAATGATTTAACCAT 1080
Db 1021 TTTTACAGAGAGCTTTGACACCGTGTGTCTGAGATGAGACATTAATGATTTAACCAT 1080
Qy 1081 TCAGATTAACCTTTATATACATGCTGTGCTCTCAATGACCAAGCAGATTCAGATTTTG 1140
Db 1081 TCAGATTAACCTTTATATACATGCTGTGCTCTCAATGACCAAGCAGATTCAGATTTTG 1140
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Db 1141 AACTTACCAGAGAGCTTTTCAAGATGATTTTGAAGAAATGTTTCCAGTTAGTAA 1200
Qy 1201 TTTGAGACACTTATCTTCAAAAAATGATTAAGAACTTTTCAAGTATGATCTCAG 1260
Db 1201 TTTGAGACACTTATCTTCAAAAAATGATTAAGAACTTTTCAAGTATGATCTCAG 1260
Qy 1261 AGAAGGATATGCTCTTCTTGGAAATATCAGATGTTAGCTGGAATTTCTTGGATCTG 1320
Db 1261 AGAAGGATATGCTCTTCTTGGAAATATCAGATGTTAGCTGGAATTTCTTGGATCTG 1320
Qy 1321 AGACATTAAGAAAACCTGCACTTGGGTTGAGATATAGTGTAAATTTGCTTCAAT 1380
Db 1321 AGACATTAAGAAAACCTGCACTTGGGTTGAGATATAGTGTAAATTTGCTTCAAT 1380
Qy 1381 ATGCTTACGACCTGTTTTCAGATGTTTACCTCCAGAGATCAGGATCTTACCTCAC 1440
Db 1381 ATGCTTACGACCTGTTTTCAGATGTTTACCTCCAGAGATCAGGATCTTACCTCAC 1440

Qy 1441 AGCAATTAATAAAGAGGTTCTTAACAAAGTCGTAAACTGGAAGCTTTGGCAAGATC 1500
Db 1441 AGCAATTAATAAAGAGGTTCTTAACAAAGTCGTAAACTGGAAGCTTTGGCAAGATC 1500
Qy 1501 AATGTTGCTTCAATCTTTTAACCTGACCTTCTGGAATGTCAGACTTTAGCAAGCTTTCT 1560
Db 1501 AATGTTGCTTCAATCTTTTAACCTGACCTTCTGGAATGTCAGACTTTAGCAAGCTTTCT 1560
Qy 1561 GATATGATCATGATCAAAATTCAGTTTCCCAACCATGGGCTGATTTCTTCCAGAGCTG 1620
Db 1561 GATATGATCATGATCAAAATTCAGTTTCCCAACCATGGGCTGATTTCTTCCAGAGCTG 1620
Qy 1621 CAGAAAGATGAGTCAATTAAGAGAGGAGCAATCCATTTCAATGTACTGTGAGCTAAGA 1680
Db 1621 CAGAAAGATGAGTCAATTAAGAGAGGAGCAATCCATTTCAATGTACTGTGAGCTAAGA 1680
Qy 1681 GAATTTGCAAAAATATATGACCAAGTATCAAGTGAAGTGTATGAGAGGCTGGCTGATCT 1740
Db 1681 GAATTTGCAAAAATATATGACCAAGTATCAAGTGAAGTGTATGAGAGGCTGGCTGATCT 1740
Qy 1741 TATAGTGTGACTACCCAGAAAGTTATAGAGAAAGCCACTAAGAGACTTTCACATGCT 1800
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Qy 1861 GCTGTGATCTGACCTGCTCTCTGCACTTACTTGAATCTGCTGCTGATCTGAGATGCTG 1920
Db 1861 GCTGTGATCTGACCTGCTCTCTGCACTTACTTGAATCTGCTGCTGATCTGAGATGCTG 1920
Qy 1921 TGCCAGTGAAGCCAGAGCTCGGCGCAGGCGCAGAGAAATATCCCTTGAAGAACTCCAAAGA 1980
Db 1921 TGCCAGTGAAGCCAGAGCTCGGCGCAGGCGCAGAGAAATATCCCTTGAAGAACTCCAAAGA 1980
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Db 1981 AACCTCGAGTTTCAATGCTTTTATTTATTTATATATGATGAACATGATTCGCTGCGGTGAAAAGT 2040
Qy 2041 GAATTTGATCTTACCTTGAAGAAAGATATATACGATTTTGTCTTCAAGAGAACTTT 2100
Db 2041 GAATTTGATCTTACCTTGAAGAAAGATATATACGATTTTGTCTTCAAGAGAACTTT 2100
Qy 2101 GTCCCTGCGAAGAGCATTTGGAAGAAATATCATCAACTGATTTGAGAGAGTTACAAGTCC 2160
Db 2101 GTCCCTGCGAAGAGCATTTGGAAGAAATATCATCAACTGATTTGAGAGAGTTACAAGTCC 2160
Qy 2161 ATCTTTGTTTGTCTCCCAACTTTGTCCAGAGTGAAGTGTGCTCATTAAGAACTGATTTT 2220
Db 2161 ATCTTTGTTTGTCTCCCAACTTTGTCCAGAGTGAAGTGTGCTCATTAAGAACTGATTTT 2220
Qy 2221 GCCCATCAATCTCTTCAAGAGATCTAATACTTAATCTCAATCTTCAAGAGAACTT 2280
Db 2221 GCCCATCAATCTCTTCAAGAGATCTAATACTTAATCTCAATCTTCAAGAGAACTT 2280
Qy 2281 ATTCAGAGACAGCATTTCCCAACAAAGTACCAAGAGCTGATGAGCTCATATGACGAGGG 2340
Db 2281 ATTCAGAGACAGCATTTCCCAACAAAGTACCAAGAGCTGATGAGCTCATATGACGAGGG 2340
Qy 2341 ACTTATTTGCAAGTGGCCCAAGAGAAAGCAAGCTGAGGCTCTTTTGGGCTTAACATTTAGA 2400
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Qy 2401 GCCGCTTTTATATGAAATTTAACTAGTCACTGAAAACAATGATGTAATTTCTTAAAAA 2460
Db 2401 GCCGCTTTTATATGAAATTTAACTAGTCACTGAAAACAATGATGTAATTTCTTAAAAA 2460
Qy 2461 AATTAGGAATTTCACTTAAGAAACATTTATTTACTTGAATGATGTAATGATGATGATGAT 2520
Db 2461 AATTAGGAATTTCACTTAAGAAACATTTATTTTACTTGAATGATGTAATGATGATGATGAT 2520

QY 2521 CGTAAAGTAACTGCTGGAGGTCCTCCATATCTTCATGCTTCAGAGAAAGCTTAAACA 2580
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 Db 2521 CCGTAAGTAACTGCTGGAGGTCCTCCATATCTTCATGCTTCAGAGAAAGCTTAAACA 2580
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 QY 2581 AAAACAATGTTTCACTGGGGAACCTAGAGCGGTGAGAGTTAGCTGCGCAGTTAGAGAC 2640
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 Db 2581 AAAACAATGTTTCACTGGGGAACCTAGAGCGGTGAGAGTTAGCTGCGCAGTTAGAGAC 2640
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 Db 2641 AGCCCAAGTCTCTGCTGTTTAACTATTATGTTTCAAAATGAACAGTCTCTTTTGAGTAA 2700
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 QY 2701 ATGCTCAGTTTTCAGCTCCCTCCACCTGCTTTCCCAATGAGATTCTGTTG 2753
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 RESULT 3
 ADU23187
 ID ADU23187 standard; cDNA; 2753 BP.
 AC ADU23187;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE Human Toll-like receptor 6 (TLR6) cDNA sequence - SEQ ID 79.
 XX
 KM screening; Toll-like receptor agonist; TLR agonist; gene; ss; TLR6.
 XX
 OS Homo sapiens.
 XX
 PN WO2004094671-A2.
 XX
 PD 04-NOV-2004.
 XX
 PF 22-APR-2004; 2004WO-US012788.
 XX
 PR 22-APR-2003; 2003US-0464586P.
 XX
 PR 22-APR-2003; 2003US-0464586P.
 XX
 PA (COLE-) COLEY PHARM GMBH.
 PA (COLE-) COLEY PHARM GROUP INC.
 XX
 PI Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
 XX
 DR WPI; 2004-795573/78.
 XX
 PT Identifying agonists of Toll-like receptor (TLR) signaling activity,
 PT useful therapeutically or prophylactically, comprises contacting an
 PT RPM1826 cell that expresses a TLR with a test compound and measuring TLR
 PT signaling activity.
 XX
 XX Disclosure; SEQ ID NO 79; 342pp; English.
 PS
 XX The invention comprises a screening method for identifying agonists of
 CC Toll-like receptor (TLR) signaling activity. The method involves
 CC contacting an RPM1826 cell (that expresses a TLR) with a test compound,
 CC and measuring a test level of TLR signaling activity, where a test level
 CC that is positive is indicative of a test compound that is a TLR agonist.
 CC The method of the invention is useful for identifying agonists of TLR.
 CC The present nucleic acid represents a TLR cDNA sequence.
 CC
 XX Sequence 2753 BP; 849 A; 559 C; 507 G; 838 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 2753; DB 13; Length 2753;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 61 AACATCATGACCAAGACAAAGAACCTATTGTTAAAGCTTCATTGTTGCTTANG 120
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 QY 121 ATCATTAATAGTTGGAACCGAATCCAGTTCTCCGACGAAATGAATTTGACATGACAG 180
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 Db 121 ATCATTAATAGTTGGAACCGAATCCAGTTCTCCGACGAAATGAATTTGACATGACAG 180
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 QY 181 TCAAAAAGAGGCTTATTCATGATTCGCAAAAGACCTACCGCTGAAAACCAAGCTTAGAT 240
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 Db 181 TCAAAAAGAGGCTTATTCATGATTCGCAAAAGACCTACCGCTGAAAACCAAGCTTAGAT 240
 |||||
 QY 241 ATGCTCAGAACTACATGCTGAGCTTCAAGTCTCTGACATGAGCTTTCTATCAGAGTTG 300
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 Db 241 ATGCTCAGAACTACATGCTGAGCTTCAAGTCTCTGACATGAGCTTTCTATCAGAGTTG 300
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 QY 301 ACAGTTTGAAGCTTTCCCATACAGAAATCCAGCTACTGTTGATTTAAGTTTTCAGATTG 360
 |||||
 Db 301 ACAGTTTGAAGCTTTCCCATACAGAAATCCAGCTACTGTTGATTTAAGTTTTCAGATTG 360
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 QY 361 AACCGAGATTAGATATTGGAATTTATCTGATATCAGTTGCAAAAGATATCCGCAAT 420
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 Db 361 AACCGAGATTAGATATTGGAATTTATCTGATATCAGTTGCAAAAGATATCCGCAAT 420
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 QY 421 CCTATTGAGTTTCAGGCAATTTAGATCTCTCAATCAATGATTTTCAAGGCCCTGCCATC 480
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 Db 421 CCTATTGAGTTTCAGGCAATTTAGATCTCTCAATCAATGATTTTCAAGGCCCTGCCATC 480
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 QY 481 TGTAAAGAAATTTGCAACTTATCACAAGCTGAATTTCTTGGAGTTAGTGTATGAAAGCTG 540
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 Db 481 TGTAAAGAAATTTGCAACTTATCACAAGCTGAATTTCTTGGAGTTAGTGTATGAAAGCTG 540
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 QY 541 CAAAAATTAGATTGCTGCGCAATTTGCTCACTTGCACTTAAGTTATCTTCTGAGATTGA 600
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 Db 541 CAAAAATTAGATTGCTGCGCAATTTGCTCACTTGCACTTAAGTTATCTTCTGAGATTGA 600
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 QY 601 AGAAATTTATATATAAAGAAATAGACAGAGAAAGCTACAAATCTGGAATSCAAAAACC 660
 |||||
 Db 601 AGAAATTTATATATAAAGAAATAGACAGAGAAAGCTACAAATCTGGAATSCAAAAACC 660
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 QY 661 CTTCACCTGTTGTTTTCACCCCAAGTATTTGCTATCCAAAGTGAACATATCAGTTAAT 720
 |||||
 Db 661 CTTCACCTGTTGTTTTCACCCCAAGTATTTGCTATCCAAAGTGAACATATCAGTTAAT 720
 |||||
 QY 721 ACTTTAGGAGTCTTACCACTGATCTATATTTAATTTGAATGATGACACTGTCAAGTTTC 780
 |||||
 Db 721 ACTTTAGGAGTCTTACCACTGATCTATATTTAATTTGAATGATGACACTGTCAAGTTTC 780
 |||||
 QY 781 ATTAATTTTATATGAACTACCGAGAGTTCAACCTTACGAATTTTACCCTCAACAC 840
 |||||
 Db 781 ATTAATTTTATATGAACTACCGAGAGTTCAACCTTACGAATTTTACCCTCAACAC 840
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 QY 841 ATGAGAAAGCACTGGAAATGCGTGTGTCAGAGTCTTTCATTTCTTTGGCCCAACCTGTG 900
 |||||
 Db 841 ATGAGAAAGCACTGGAAATGCGTGTGTCAGAGTCTTTCATTTCTTTGGCCCAACCTGTG 900
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 QY 901 GAATATCTCAATTTTAACTAATTTAACAATTAATGAAAGCAATTCGTGAAGAAATTTACT 960
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 Db 901 GAATATCTCAATTTTAACTAATTTAACAATTAATGAAAGCAATTCGTGAAGAAATTTACT 960
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 |||||
 Db 961 TATTTCTAAAGCACTGAAAGCAATGACATAGAACATATCAAGAACCAAGTTTCTG 1020
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 QY 1021 TTTTTCACAGACAGCTTTGTACACCGTGTGTTTCTGAGATGAACATATGATGTTAACAT 1080
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 Db 1021 TTTTTCACAGACAGCTTTGTACACCGTGTGTTTCTGAGATGAACATATGATGTTAACAT 1080
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 Db 1081 TCAATATACACTTTTATATACATGCTGTGTCTTATGATGACCAAGCAATTCAGTTTGG 1140
 |||||
 QY 1141 AACTTACCCGAGACGTTTTCACAGATAGTATTTTGAATAATGTTCCACGTTAGTTAA 1200
 |||||

Db	1141	AACCTTACCAGAAACGTTTTCACAGATAGTATTTTGAATAATGTTCCAGCTTAGTTAA	1200
Qy	1201	TTGGAGACACTTATCTTCAAAAATAATGATTTAAAGAAGCTTTTCAAGTAGTCTCATG	1260
Db	1201	TTGGAGACACTTATCTTCAAAAATAATGATTTAAAGAAGCTTTTCAAGTAGTCTCATG	1260
Qy	1261	ACGAAGATATGCTCTTTGGAAATACCTGATGTTAGCTGGAAATCTTTGGAAATCTGGT	1320
Db	1261	ACGAAGGATATGCTCTTTGGAAATACCTGATGTTAGCTGGAAATCTTTGGAAATCTGGT	1320
Qy	1321	AGACATAAGAAAACTGCATCTGGGTTGAGATATAGTGGTGAATTTGTAATTTGCTTCAAT	1380
Db	1321	AGACATAAGAAAACTGCATCTGGGTTGAGATATAGTGGTGAATTTGTAATTTGCTTCAAT	1380
Qy	1381	ATGCTTACTGACTCTGTTTTCAGATGTTTACCTCCAGATCAAGGTACCTTGATCTTCAC	1440
Db	1381	ATGCTTACTGACTCTGTTTTCAGATGTTTACCTCCAGATCAAGGTACCTTGATCTTCAC	1440
Qy	1441	AGCAATAAATPAAGAGCGCTTCTTAACAAGTCGTAAATCTGGAAGCTTTGCAAGAACTC	1500
Db	1441	AGCAATAAATPAAGAGCGCTTCTTAACAAGTCGTAAATCTGGAAGCTTTGCAAGAACTC	1500
Qy	1501	AATGTTGCTTTCATCTTTTAACTGACCTTCCAGCCAGTGGCTGATTTCTTCCAGAGCTGC	1560
Db	1501	AATGTTGCTTTCATCTTTTAACTGACCTTCCAGTATGGCAGCTTTAGACAGCTTTCCT	1560
Qy	1561	GTAATGATCATGTGATCACAATTCAGTTCCTCCAGCCAGTGGCTGATTTCTTCCAGAGCTGC	1620
Db	1561	GTAATGATCATGTGATCACAATTCAGTTCCTCCAGCCAGTGGCTGATTTCTTCCAGAGCTGC	1620
Qy	1621	CAGAAATGAGGTCAATPAAGACAGGGGACAAATCCATTCGAATGTAAGCTGTGACTPAAGA	1680
Db	1621	CAGAAATGAGGTCAATPAAGACAGGGGACAAATCCATTCGAATGTAAGCTGTGACTPAAGA	1680
Qy	1681	GAAATTTGTCAAAAAATATGACCAACAATATCAAGTGAAGTTTGAAGGGCTGGCCGTGATTCCT	1740
Db	1681	GAAATTTGTCAAAAAATATGACCAACAATATCAAGTGAAGTTTGAAGGGCTGGCCGTGATTCCT	1740
Qy	1741	TATAAGTGTGACTACCCAGAAAAGTATATAGGAAACCCACTPAAGAGACCTTTCACATGCT	1800
Db	1741	TATAAGTGTGACTACCCAGAAAAGTATATAGGAAACCCACTPAAGAGACCTTTCACATGCT	1800
Qy	1801	GAAATATCTCTGCACATATACCTGTGATCGTCACATCGGTGCCACATGCTGGTGTG	1860
Db	1801	GAAATATCTCTGCACATATACCTGTGATCGTCACATCGGTGCCACATGCTGGTGTG	1860
Qy	1861	GCTGTGATCTGTGACCTCCCTCTGTGATCTACTTTGATCTGCCCCGTGATCTCAGATGGTG	1920
Db	1861	GCTGTGATCTGTGACCTCCCTCTGTGATCTACTTTGATCTGCCCCGTGATCTCAGATGGTG	1920
Qy	1921	TGCCAGTGGAACCCAGACTCGGGGACAGGGGACAGAAATACCTTGTGAAGAACTCCAAGA	1980
Db	1921	TGCCAGTGGAACCCAGACTCGGGGACAGGGGACAGAAATACCTTGTGAAGAACTCCAAGA	1980
Qy	1981	AACCTTCAGTTTCATGCTTTTATTTTATATATAGTGAACAATGATTCGCCCTGGGTGAAAAGT	2040
Db	1981	AACCTTCAGTTTCATGCTTTTATTTTATATATAGTGAACAATGATTCGCCCTGGGTGAAAAGT	2040
Qy	2041	GAAATTTGTGTAACCTTACCTTGAAGAAAAGATATACAGATTTGTCTTCATGAGAGGAACCTTT	2100
Db	2041	GAAATTTGTGTAACCTTACCTTGAAGAAAAGATATACAGATTTGTCTTCATGAGAGGAACCTTT	2100
Qy	2101	GTCCTCGGCAAGAGATGTTGGAAAAATATCATCAACTGCATTTGAGAAAGATTACAAGTCC	2160
Db	2101	GTCCTCGGCAAGAGATGTTGGAAAAATATCATCAACTGCATTTGAGAAAGATTACAAGTCC	2160
Qy	2161	ATCTTTGTTTGTCTCCCAACTTTGTGCAAGATGAGTGGTGCATTAAGAACTCTATTTT	2220
Db	2161	ATCTTTGTTTGTCTCCCAACTTTGTGCAAGATGAGTGGTGCATTAAGAACTCTATTTT	2220
Qy	2221	GCCCATCACATCTCTTTCATGAAAGATATATTAATCTTATCTCATCTTACTGGAACCC	2280
Db	2221	GCCCATCACATCTCTTTCATGAAAGATATATTAATCTTATCTCATCTTACTGGAACCC	2280

QY	2281	ATTCCACGAAACAGCATTTCCCAACAAGTACCACAAGCTGAAAGGCTCTTCATAGCCAGGG	2340
Db	2281	ATTCCACGAAACAGCATTTCCCAACAAGTACCACAAGCTGAAAGGCTCTTCATAGCCAGGG	2340
QY	2341	ACTTATTGACGTGGCCCAAGAGAAAAAGCAAAAGTGGGCTCTTTGGGCTAACATTAGA	2400
Db	2341	ACTTATTGACGTGGCCCAAGAGAAAAAGCAAAAGTGGGCTCTTTGGGCTAACATTAGA	2400
QY	2401	GCCGCTTTTAAATGAAATTAACTCTAGTCACTGAAAACAATGATGGAATCTTAAAA	2460
Db	2401	GCCGCTTTTAAATGAAATTAACTCTAGTCACTGAAAACAATGATGGAATCTTAAAA	2460
QY	2461	AATTTAGGAATTCAACTTAGAAGAACCTTTACTTGATGATGATGGTAATAGACAGT	2520
Db	2461	AATTTAGGAATTCAACTTAGAAGAACCTTTACTTGATGATGATGGTAATAGACAGT	2520
QY	2521	CGTAGTAGACGTCTGAGAGTGCCCTCCATTATCTCATGCTCTCAGGAAAGACTTAA	2580
Db	2521	CGTAGTAGACGTCTGAGAGTGCCCTCCATTATCTCATGCTCTCAGGAAAGACTTAA	2580
QY	2581	AAACAAATGTTTCATCTGGGGAACCTGAGCTAGGCGGTGAGGTTAAGCTGCCAGTTAGAGAC	2640
Db	2581	AAACAAATGTTTCATCTGGGGAACCTGAGCTAGGCGGTGAGGTTAAGCTGCCAGTTAGAGAC	2640
QY	2641	AGCCCAAGCTCTTCGAGTTTAAATCATTAATGTTTCAAAATGAAACAGTCTCTTTGAGTAA	2700
Db	2641	AGCCCAAGCTCTTCGAGTTTAAATCATTAATGTTTCAAAATGAAACAGTCTCTTTGAGTAA	2700
QY	2701	ATGCTCAGTTTTTACGCTCTCTCCACTCTGCTTTCCCAATGGAATTCGTGTTG	2763
Db	2701	ATGCTCAGTTTTTACGCTCTCTCCACTCTGCTTTCCCAATGGAATTCGTGTTG	2763

RESULT 4
 ADX06215
 ID ADX06215 standard; DNA; 2753 BP.
 AC
 AC ADX06215;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 780.
 XX
 KW cytosstatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2005012875-A2.
 XX
 PD 10-FEB-2005.
 XX
 PF 29-JUL-2004; 2004WO-US024424.
 XX
 PR 29-JUL-2003; 2003US-0490890P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
 XX
 DR WPI; 2005-163068/17.
 XX
 DR P-PSDB; ADX06216.
 PT Biomarkers useful for predicting or determining the response of a mammal
 PT to a cancer treatment comprising administration of a modulator of cyclin-
 PT dependent kinase activity.
 XX
 PS Claim 5; SEQ ID NO 780; 141bp; English.
 XX
 CC This invention describes a novel method of predicting or determining
 CC whether a mammal will respond or is responding to an anti-cancer agent
 CC that modulates cyclin-dependent kinase (cdk) activity. The method
 CC comprises measuring the level of one or more biomarkers selected from

CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
 CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
 CC invention is utilized in a kit for determining or predicting whether
 CC patient would be susceptible or resistant to treatment by an agent.
 CC modulating cdk activity. The invention also describes a method for
 CC utilizing individualized genetic profiles for treating diseases and
 CC disorders based on patient's response and molecular level, specialized
 CC microarrays comprising the biomarkers described, antibodies directed
 CC against the biomarkers and a cell culture model to identify biomarkers.
 CC The cdk modulator is preferably N-5-[(5-(1,1-dimethylethyl)-2-
 CC oxazolyl)methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
 CC tartaric acid salt. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from Wipo at ftp.wipo.int/pub/published/pct sequences. This
 CC sequence encodes a biomarker used in the method of the invention.

XX Sequence 2753 BP, 849 A; 559 C; 507 G; 838 T; 0 U; 0 Other;

Query Match 100.0%; Score 2753; DB 14; Length 2753;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAATTTGAGCTCATATCAAGATGCTGTGAGAGAGAACACCCTTAGAGATGACCACTGC 60
 Db 1 AGAATTTGAGCTCATATCAAGATGCTGTGAGAGAGAACACCCTTAGAGATGACCACTGC 60
 QY 61 AACATCAGACCCAAAGACAAAGAACCTATGTTAAAGCTTTCATTTTGTGCTTATG 120
 Db 61 AACATCAGACCCAAAGACAAAGAACCTATGTTAAAGCTTTCATTTTGTGCTTATG 120
 QY 121 ATCAATATAGTTGGAACAGAAATCCAGTTCTCCGACGGAATGAATTTGACATAGCAAG 180
 Db 121 ATCAATATAGTTGGAACAGAAATCCAGTTCTCCGACGGAATGAATTTGACATAGCAAG 180
 QY 181 TCAAAAAGAGGCTTATTCATGTTCCAAAAGACCTACCGCTGAAAAACCAAGCTTGAAT 240
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 Db 301 ACAGTTTGGAGACTTCCCATACAGAAATCCAGTACTGATTTAAAGTGTTCAGATTTC 360
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 Db 421 CCTATTTGAGATTTGAGGCAATTTAGATCTCTCATTCATGATTTCAAGGCCCTGCCATC 480
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 Db 481 TGTAAAGAAATTTGGCAATTTATCAACAGTGAATTTCTGGGATTTGAGTATGAGAGTGC 540
 QY 541 CAAAATTTAGATTGCTGCCAATTTGCTCACTTGCATCTAAGTTATATCTTCTGGAATTTA 600
 Db 541 CAAAATTTAGATTGCTGCCAATTTGCTCACTTGCATCTAAGTTATATCTTCTGGAATTTA 600
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 Db 601 AGAAATTTATATTAAGAAATGAGACAGAAAGTCTACAAATTTCTGATGCAAAAAACC 660
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 Db 661 CTTCACCTTTTTCACCCAACTAGTTATTCGCTATCCAAAGTGAACATACATGATTAAT 720
 QY 721 ACTTTAGGGTGTTCACAACTGATCTAATATTAATTTGAATGATGACACATGTCAGATTTC 780
 Db 721 ACTTTAGGGTGTTCACAACTGATCTAATATTAATTTGAATGATGACACATGTCAGATTTC 780

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 Db 1021 TTTTCACAGACAGCTTTGTATCACCGTGTCTGTGATGATGACATTTATGATTAACAT 1080
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Db 2641 AGCCAGTCTCTTCTGGTTTATCATATGTTTCAATTTGAATGAAACAGTCTCTTTGAGTAA 2700
Qy 2701 ATGCTCAGTTTTCAGTCTCTCTCCACTGCTTCCCAATGAAATGATTCGTTG 2753
Db 2701 ATGCTCAGTTTTCAGTCTCTCTCTCCACTGCTTCCCAATGAAATGATTCGTTG 2753

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RESULT 5
AAD26300
ID AAD26300 standard; cDNA; 2760 BP.
XX
XX AAD26300;
AC 26-MAR-2002 (first entry)
DT
DE Human DNAX Toll like receptor (DTLR) 9 cDNA #2.
XX
XX Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW interleukin 1; IL-1; screening; immunomodulator; ss.

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XX Homo sapiens.
OS Location/Qualifiers
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FT /*tag= b
FT mat_peptide 161..2455
FT /*tag= c
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PD
XX 23-MAY-2001; 2001WO-US016766.
PF
XX 25-MAY-2000; 2000US-0207558P.
PR
XX (SCHE ) SCHERING CORP.
PA
XX Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWX, Liu Y,
PI WPI; 2002-083085/11.
XX P-PSDB; AAE16109, AAE16112.
XX
XX New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
XX
XX Claim 16; Page 72-75; 297pp; English.
PS
XX
XX The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTLR) protein and their corresponding
CC nucleic acids. The DTLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTLR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTLR or its various fragments. The
CC purified DTLR can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression
CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTLR or cells that express it. The present sequence is
CC human DTLR9 cDNA
XX
XX
SQ Sequence 2760 BP; 850 A; 560 C; 511 G; 838 T; 0 U; 1 Other;
Query Match 99.8%; Score 2748.8; DB 6; Length 2760;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 3; Indels 0; Gaps 0;
Matches 2750; Conservative 0;
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Db 62 AACATCATGACCAAGAAAGAAACCTTATTTGTTAAAGCTTCCATTTTGTCTTATG 121
Qy 121 ATCATTAATAGTTTGAACCAAGATCCAGTTCCTCCGCGGAAATGAATTTGAGTAGAAG 180
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Db 602 AGAAATTTATATATATAAAGAAATGAGACAGAAAGTCTACAAATCTGAAATCAAAAACC 661
QY 661 CTTCACCTTGTCTTTCACCCCACTGATTTATTCGCTATCAGAGTCAATCAGATTAT 720
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QY 1141 AACTTTACCGAAGCGTTTTCACAGATGATATTTTGAAGAAATGTTTCCAGTTAGTAA 1200
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RESULT 6

ADU23186 standard; cDNA; 2760 BP.

ADU23186;

27-JAN-2005 (first entry)

Human Toll-like receptor 6 (TLR6) cDNA sequence - SEQ ID 78.

screening; Toll-like receptor agonist; TLR agonist; gene; ss; TLR6.

Homo sapiens.

WO2004094671-A2.

04-NOV-2004.

22-APR-2004; 2004WO-US012788.

22-APR-2003; 2003US-0464586P.

22-APR-2003; 2003US-0464588P.

(COLE-) COLEY PHARM GMBH.

(COLE-) COLEY PHARM GROUP INC.

Volmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;

MPI, 2004-795573/78.

Identifying agonists of Toll-like receptor (TLR) signaling activity, useful therapeutically or prophylactically, comprises contacting an RPM1826 cell that expresses a TLR with a test compound and measuring TLR signaling activity.

Disclosure; SEQ ID NO 78; 342pp; English.

The invention comprises a screening method for identifying agonists of Toll-like receptor (TLR) signaling activity. The method involves contacting an RPM1826 cell (that expresses a TLR) with a test compound, and measuring a test level of TLR signaling activity, where a test level that is positive is indicative of a test compound that is a TLR agonist. The method of the invention is useful for identifying agonists of TLR. The present nucleic acid represents a TLR cDNA sequence.

SQ Sequence 2760 BP; 850 A; 560 C; 511 G; 838 T; 0 U; 1 Other;

Query Match 99.8%; Score 2748.8; DB 13; Length 2760;

Best Local Similarity 99.9%; Pred. No. 0; Matches 2750; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 AGAATTTGAGTCAATTCAGATGCTCTGAAGAAACAAACCTTTAGATAGCACTGC 60
2 AGAATTTGAGTCAATTCAGATGCTCTGAAGAAACAAACCTTTAGATAGCACTGC 61
QY 61 AACATCATGACCAAGCAAGAACTATGTTAAAGCTCCATTTGTTGGCTTAATG 120
Db 62 AACATCATGACCAAGCAAGAACTATGTTAAAGCTTCATTTGTTGGCTTAATG 121
QY 121 ATCATTAATAGTTGGAACGAGATCCAGTCTCCAGCGAAATGAATTCAGTACAG 180
Db 122 ATCATTAATAGTTGGAACGAGATCCAGTCTCCAGCGAAATGAATTCAGTACAG 181
QY 181 TCAAAAGAGGTCCTTATTCATGTTCCAAAAGACCTACCGCTGAAAACCAAGCTT 240
Db 182 TCAAAAGAGGTCCTTATTCATGTTCCAAAAGACCTACCGCTGAAAACCAAGCTT 241
QY 241 ATGCTCAGACTCATGCTGAGCTCAGGCTCTGACATGAGCTTCTATCAGATTTG 300
Db 242 ATGCTCAGACTCATGCTGAGCTCAGGCTCTGACATGAGCTTCTATCAGATTTG 301
QY 301 ACAGTTTGAAGCTTCCCATTAAGAGATCCAGCTCTTGAATTTAGTGTTCAGTTG 360
Db 302 ACAGTTTGAAGCTTCCCATTAAGAGATCCAGCTCTTGAATTTAGTGTTCAGTTG 361
QY 361 AACAGAGTTTGAATATTTGATTTATCTATATATCAGTTGCAAAAGATATCCTGC 420
Db 362 AACAGAGTTTGAATATTTGATTTATCTATATATCAGTTGCAAAAGATATCCTGC 421
QY 421 CCTATGAGTTTCAGGCAATTTAGATCTCCATTCATTAATTTCAAGGCTCCGCTC 480
Db 422 CCTATGAGTTTCAGGCAATTTAGATCTCCATTCATTAATTTCAAGGCTCCGCTC 481
QY 481 TGTAAAGAAATTTGGCAATTTATCAACAAGTGAATTTCTGGAGTTGAGTCTAG 540
Db 482 TGTAAAGAAATTTGGCAATTTATCAACAAGTGAATTTCTGGAGTTGAGTCTAG 541
QY 541 CAAAATTAAGATTGCTGCTCCAAATTTGCTGATTCGATTAATTCCTTGGATT 600
Db 542 CAAAATTAAGATTGCTGCTCCAAATTTGCTGATTCGATTAATTCCTTGGATT 601
QY 601 AGAAATTTAATTAATTAAGAAATGAGACAGAAAGTCTAGAAATTTCTAGCAAAA 660
Db 602 AGAAATTTAATTAATTAAGAAATGAGACAGAAAGTCTAGAAATTTCTAGCAAAA 661
QY 661 CTTCACTTGTGTTTTCACCAACTAGTTTATTCGCTATCCAAGTGAACATATCG 720
Db 662 CTTCACTTGTGTTTTCACCAACTAGTTTATTCGCTATCCAAGTGAACATATCG 721
QY 721 ACTTTAGGCTGCTTCAACTGATCTAATATTAATTTGAATGATGACAACTGCA 780
Db 722 ACTTTAGGCTGCTTCAACTGATCTAATATTAATTTGAATGATGACAACTGCA 781
QY 781 ATTAATTTTATTAATTAAGAACTGACAGAGGTTCAACCTTACGAAATTTTAA 840
Db 782 ATTAATTTTATTAATTAAGAACTGACAGAGGTTCAACCTTACGAAATTTTAA 841
QY 841 ATAGAAAGCACTTGAATATGCTGCTGATGAGCTTCAATTTCTTTGGCCCAAC 900
Db 842 ATAGAAAGCACTTGAATATGCTGCTGATGAGCTTCAATTTCTTTGGCCCAAC 901
QY 901 GAATATCTCAATTTTACAAATTTAACTAATATGAAAGCATTTCTGAAAGAA 960
Db 902 GAATATCTCAATTTTACAAATTTAACTAATATGAAAGCATTTCTGAAAGAA 961
QY 961 TATTTCTAAAGCACTTGAAGCAATGACATTAAGCAATATCAGCAAGCAAGTT 1020
Db 962 TATTTCTAAAGCACTTGAAGCAATGACATTAAGCAATATCAGCAAGCAAGTT 1021

QY 1021 TTTTCACAGACAGCTTTTGACACCGTGTCTGAGATGAACTTATGATGTTAAACATT 1080
 DB 1022 TTTTCACAGACAGCTTTTGACACCGTGTCTGAGATGAACTTATGATGTTAAACATT 1081
 QY 1081 TCAGATACACCTTTTATACACATGCTGTGTCTCATGACCAAGACATTCAGTTTGTG 1140
 DB 1082 TCAGATACACCTTTTATACACATGCTGTGTCTCATGACCAAGACATTCAGTTTGTG 1141
 QY 1141 AACTTACCCAGAAAGCTTTTTCACATGATATTTTGGAAAAATGTTCCACGTTAGTTAA 1200
 DB 1142 AACTTACCCAGAAAGCTTTTTCACATGATATTTTGGAAAAATGTTCCACGTTAGTTAA 1201
 QY 1201 TTGGACACCTTATCTTCAAAAAATGATTTAAAGACCTTTTCAAGTAGTCTCAG 1260
 DB 1202 TTGGACACCTTATCTTCAAAAAATGATTTAAAGACCTTTTCAAGTAGTCTCAG 1261
 QY 1261 AGGAAAGATATGCTCTTCTTGGAAATCTGATGTTAGCTGGAATCTTGGAACTGTGT 1320
 DB 1262 AGGAAAGATATGCTCTTCTTGGAAATCTGATGTTAGCTGGAATCTTGGAACTGTGT 1321
 QY 1321 AGACATTAAGAAACCTGCACTGGGTGAGAGATATAGTGTATTAATTTGCTTCAAT 1380
 DB 1322 AGACATTAAGAAACCTGCACTGGGTGAGAGATATAGTGTATTAATTTGCTTCAAT 1381
 QY 1381 ATGCTTACCTGACTGTTTTCAGATGTTTACCTCCAGAGATCAAGGTACTGATCTGAC 1440
 DB 1382 ATGCTTACCTGACTGTTTTCAGATGTTTACCTCCAGAGATCAAGGTACTGATCTGAC 1441
 QY 1441 AGCAATTAATTAAGAGCGTCTTAAACAAGTCTTAAACCTGGAAGCTTTGGACAAGCTC 1500
 DB 1442 AGCAATTAATTAAGAGCGTCTTAAACAAGTCTTAAACCTGGAAGCTTTGGACAAGCTC 1501
 QY 1501 AATGTGCTTCAATCTTTTAACTGACCTTCTGATGTGGAGCTTTAGACGCTTTCT 1560
 DB 1502 AATGTGCTTCAATCTTTTAACTGACCTTCTGATGTGGAGCTTTAGACGCTTTCT 1561
 QY 1561 GTATTGATCATGATCAAAATTCAGTTTCCACCGATGGGCTGATTTCTCCAGAGCTGC 1620
 DB 1562 GTATTGATCATGATCAAAATTCAGTTTCCACCGATGGGCTGATTTCTCCAGAGCTGC 1621
 QY 1621 CAGAAATGAGGTCAATTAAGACAGGGGCAATCCATTCATGACCTGTAGAGTAA 1680
 DB 1622 CAGAAATGAGGTCAATTAAGACAGGGGCAATCCATTCATGACCTGTAGAGTAA 1681
 QY 1681 GAATTTGTCAAAATATAGCAAGTATCAAGTAAAGTGTAGAGGGCTGGCTGATTTCT 1740
 DB 1682 GAATTTGTCAAAATATAGCAAGTATCAAGTAAAGTGTAGAGGGCTGGCTGATTTCT 1741
 QY 1741 TATAGTGTGATCTTCCAGAAAGTTATAGAGAAAGCCCACTTAAGACTTTCACTGTCT 1800
 DB 1742 TATAGTGTGATCTTCCAGAAAGTTATAGAGAAAGCCCACTTAAGACTTTCACTGTCT 1801
 QY 1801 GAATTTATCTTCAACATTAATCTGCTGATCGTCAACATCGGTGCCACCATGCTGGTGTG 1860
 DB 1802 GAATTTATCTTCAACATTAATCTGCTGATCGTCAACATCGGTGCCACCATGCTGGTGTG 1861
 QY 1861 GCTGTGACTGATCTTCCCTCTGCAATCTTGTGATCTGCTGTGATCTCAGATGCTG 1920
 DB 1862 GCTGTGACTGATCTTCCCTCTGCAATCTTGTGATCTGCTGTGATCTCAGATGCTG 1921
 QY 1921 TTGCAGTGGACCCGACCTGGGCGAGGGCCAGAAACATACCTTAAGAAATCCCAAGA 1980
 DB 1922 TTGCAGTGGACCCGACCTGGGCGAGGGCCAGAAACATACCTTAAGAAATCCCAAGA 1981
 QY 1981 AACCTCAGTTTCAATGCTTTTATTTATATAGTGAACATGATTCCTGCTGGGTGAAGT 2040
 DB 1982 AACCTCAGTTTCAATGCTTTTATTTATATAGTGAACATGATTCCTGCTGGGTGAAGT 2041
 QY 2041 GAATTTGTAATCTTCAATGAAAGAAATATACGATTTTGTCTTCAATGAGAACTTT 2100
 DB 2042 GAATTTGTAATCTTCAATGAAAGAAATATACGATTTTGTCTTCAATGAGAACTTT 2101

QY 2101 GTCCCTGGCAGAGCATTTGTGGAAAAATATCATCACTGCATTTGAGAAGTTACAGTCC 2160
 DB 2102 GTCCCTGGCAGAGCATTTGTGGAAAAATATCATCACTGCATTTGAGAAGTTACAGTCC 2161
 QY 2161 ATCTTTGTTTGTCTCCCACTTTGTCCAGAGTGTGTGCTCAATTCAGAACTTATTT 2220
 DB 2162 ATCTTTGTTTGTCTCCCACTTTGTCCAGAGTGTGTGCTCAATTCAGAACTTATTT 2221
 QY 2221 GCCCATCAATCTCTTTCATGAAAGATCTAATACTTAATCTCATCTTATGGAACCC 2280
 DB 2222 GCCCATCAATCTCTTTCATGAAAGATCTAATACTTAATCTCATCTTATGGAACCC 2281
 QY 2281 ATTCACAGAAACAGATTCCTCCCAACAGTACCAAGAGCTGAAGGCTCTATGACGAGCG 2340
 DB 2282 ATTCACAGAAACAGATTCCTCCCAACAGTACCAAGAGCTGAAGGCTCTATGACGAGCG 2341
 QY 2341 ACTTATTTGCAATGAGCCCAAGAGAAAGCAAACTGTGGCTCTTTTGGCTTAACATTAGA 2400
 DB 2342 ACTTATTTGCAATGAGCCCAAGAGAAAGCAAACTGTGGCTCTTTTGGCTTAACATTAGA 2401
 QY 2401 GCCGCTTTTAAATATGAATTAACACTAGTCACTGAAAAATGATGTGAATCTTAAAA 2460
 DB 2402 GCCGCTTTTAAATATGAATTAACACTAGTCACTGAAAAATGATGTGAATCTTAAAA 2461
 QY 2461 AATTAGGAAATTCACCTTAAGAAACATTAATTTTACTTGGATGATGTGAATGACAGT 2520
 DB 2462 AATTAGGAAATTCACCTTAAGAAACATTAATTTTACTTGGATGATGTGAATGACAGT 2521
 QY 2521 CGTAATGTAATCTGTGAGAGTGCCTCATTAATCTCATGCTTCCAGAAAGCTTTACAA 2580
 DB 2522 CGTAATGTAATCTGTGAGAGTGCCTCATTAATCTCATGCTTCCAGAAAGCTTTACAA 2581
 QY 2581 AAACAATGTTTCAATGTGGGGAATCTGAGCTGAGCGGTGAGTTAGCTCCAGTTTGAAC 2640
 DB 2582 AAACAATGTTTCAATGTGGGGAATCTGAGCTGAGCGGTGAGTTAGCTCCAGTTTGAAC 2641
 QY 2641 AGCCAGTCTCTGCTGGTTTATCATTAATGTTTCAATTTGAACAGTCTTTTGAATTA 2700
 DB 2642 AGCCAGTCTCTGCTGGTTTATCATTAATGTTTCAATTTGAACAGTCTTTTGAATTA 2701
 QY 2701 ATGCTCAATTTTTCAGCTCTCTCCACTGCTTCCCAATGATGATCTGTG 2753
 DB 2702 ATGCTCAATTTTTCAGCTCTCTCTCCACTGCTTCCCAATGATGATCTGTG 2754

RESULT 7
 AAA39809
 ID AAA39809 standard; cDNA; 2760 BP.
 XX
 AC AAA39809;
 XX
 DT 22-SEP-2000 (first entry)
 XX
 DE Human Toll-like receptor TLR6 cDNA.
 XX
 KM Toll-like receptor; TLR6, human; anti-infectious; treatment; infection;
 XX transcription factor; NF-kappaB; immune response; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 68..2458
 FT /*tag= a
 FT /product= "TLR6"
 XX
 PN WO200024776-A1.
 XX
 PD 04-MAY-2000.
 XX
 PF 26-OCT-1999; 99WO-JP005917.
 XX
 PR 26-OCT-1998; 98JP-00304110.
 XX

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Akira S, Takeuchi O;

XX WPI; 2000-350697/30.

DR P-PSDB; AAY8054.

XX Toll-like receptor TLR6 molecule and encoded gene, participating in
XX signal transduction of initial immune response, applicable e.g. in
XX treating infections.

XX Claim 4; Page 25-27; 35PD; Japanese.

XX This invention describes a novel toll-like receptor TLR6 which has
XX antifunction activity. The protein and its encoded gene have clinical
XX use e.g. in treating infections. Toll family receptors are related to
XX transcription factor NF-kappaB and regulate the expression of various
XX genes participating in the immune response. This sequence encodes the
XX human TLR6 protein which is described in the method of the invention

XX Sequence 2760 BP; 850 A; 561 C; 511 G; 837 T; 0 U; 1 Other;

Query Match 99.8%; Score 2747.2; DB 3; Length 2760;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 AGAATTTGAGCTCATATCAAGATGCTGCGAAGAAGAACACCTTAGATAGCCACTGC 60
DB 2 AGAATTTGAGCTCATATCAAGATGCTGCGAAGAAGAACACCTTAGATAGCCACTGC 61
QY 61 AACATCATGACCAAGACCAAGAACCTATTGTTAAAGCTTCCATTGTTGCTTATG 120
DB 62 AACATCATGACCAAGACCAAGAACCTATTGTTAAAGCTTCCATTGTTGCTTATG 121
QY 121 ATCATATATGTTGGAACCAAGATCCAGTCTCCGACGGAATGAAATTTGCAAGACAG 180
DB 122 ATCATATATGTTGGAACCAAGATCCAGTCTCCGACGGAATGAAATTTGCAAGACAG 181
QY 181 TCAAAAAGAGGCTTATTCATCTCCAAAAGACCTACCGCTGAAAACCAAGCTTATGAT 240
DB 182 TCAAAAAGAGGCTTATTCATCTCCAAAAGACCTACCGCTGAAAACCAAGCTTATGAT 241
QY 241 ATGCTTCAGAACTACATCGCTGAGCTTCAGGCTCTGACATGAGCTTTCTACAGATG 300
DB 242 ATGCTTCAGAACTACATCGCTGAGCTTCAGGCTCTGACATGAGCTTTCTACAGATG 301
QY 301 ACAGTTTGGAGCTTCCCAATAACAGATCCAGCTACCTTGAATTAAGTGTTCAGATTC 360
DB 302 ACAGTTTGGAGCTTCCCAATAACAGATCCAGCTACCTTGAATTAAGTGTTCAGATTC 361
QY 361 AACCGAGATTGGAATTTGGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTT 420
DB 362 AACCGAGATTGGAATTTGGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTT 421
QY 421 CCTATTGAGATTGAGGATTTAGATCTCTCATTCATCAATGATTTCCAGGCTGCGCATC 480
DB 422 CCTATTGAGATTGAGGATTTAGATCTCTCATTCATCAATGATTTCCAGGCTGCGCATC 481
QY 481 TGTAAAGAAATTTGGCAACTTATCAACAAGTGAATTTCTGGGATGAGTGTATGAAGCTG 540
DB 482 TGTAAAGAAATTTGGCAACTTATCAACAAGTGAATTTCTGGGATGAGTGTATGAAGCTG 541
QY 541 CAAAATTTAGATTTGCTGCAATTTGCTCACTTGCACTAAGTTATATCTTTCTGAGTTTA 600
DB 542 CAAAATTTAGATTTGCTGCAATTTGCTCACTTGCACTAAGTTATATCTTTCTGAGTTTA 601
QY 601 AGAATTTATATATATAAAGAAATGAGACAGAAAGCTACAAATTTGGAATGCAAAAAC 660
DB 602 AGAATTTATATATATAAAGAAATGAGACAGAAAGCTACAAATTTGGAATGCAAAAAC 661
QY 661 CTTCACCTTGTGTTTTCACCAACTAGTTATTTGCTATCCAAAGTGAACATATCAGTTAAT 720
DB 662 CTTCACCTTGTGTTTTCACCAACTAGTTATTTGCTATCCAAAGTGAACATATCAGTTAAT 721
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QY 721 ACTTAGGGTGCTTACAACTGACTAATATTAATTGAATGACCAACTGTCAAGTTTC 780
DB 722 ACTTAGGGTGCTTACAACTGACTAATATTAATTGAATGACCAACTGTCAAGTTTC 781
QY 781 ATTAATTTTATACGAACCTACAGAGGTTCAACCTTACGTGAATTTTAACTCAACAC 840
DB 782 ATTAATTTTATACGAACCTACAGAGGTTCAACCTTACGTGAATTTTAACTCAACAC 841
QY 841 ATAGAAACGACTTGGAAATGCTGTGAGAGTCTTCAATTTCTTGGGCCCAACCTGTG 900
DB 842 ATAGAAACGACTTGGAAATGCTGTGAGAGTCTTCAATTTCTTGGGCCCAACCTGTG 901
QY 901 GAATATCTCAATATTTTACAAATTTTAACTAATATTAAGACATTCGTGAAGAAATTTACT 960
DB 902 GAATATCTCAATATTTTACAAATTTTAACTAATATTAAGACATTCGTGAAGAAATTTACT 961
QY 961 TATTTTAAACGACTTGAAGACCTTGACATTAAGACATACAGAACCAAGTTTCTG 1020
DB 962 TATTTTAAACGACTTGAAGACCTTGACATTAAGACATTAAGACCAAGTTTCTG 1021
QY 1021 TTTTCACAGACGCTTTGTACACGCTGTTTCTGAGATGAACATTAATGATTAACAT 1080
DB 1022 TTTTCACAGACGCTTTGTACACGCTGTTTCTGAGATGAACATTAATGATTAACAT 1081
QY 1081 TCAGATACACCTTTTATACACATGCTGTGCTCATGACACCAAGACATTCAGTTTTCG 1140
DB 1082 TCAGATACACCTTTTATACACATGCTGTGCTCATGACACCAAGACATTCAGTTTTCG 1141
QY 1141 AACTTTACCAGAACGTTTTCACAGATATATTTTGAAGAAATGTTCCAGCTTATGTTAA 1200
DB 1142 AACTTTACCAGAACGTTTTCACAGATATATTTTGAAGAAATGTTCCAGCTTATGTTAA 1201
QY 1201 TTGAGACACTATCTTCAAAAAAATGATTAATAAGCCTTTTCAAGTAGTCTATG 1260
DB 1202 TTGAGACACTATCTTCAAAAAAATGATTAATAAGCCTTTTCAAGTAGTCTATG 1261
QY 1261 ACAGAGATATGCTCTTTTGAAGAAATCTGATGTTTACCTGGAATTTCTTGGAACTGCT 1320
DB 1262 ACAGAGATATGCTCTTTTGAAGAAATCTGATGTTTACCTGGAATTTCTTGGAACTGCT 1321
QY 1321 AGACATTAAGAAACCTGACCTTGGGTGAGATATAGTGTGTTAAATTTGCTTCAAT 1380
DB 1322 AGACATTAAGAAACCTGACCTTGGGTGAGATATAGTGTGTTAAATTTGCTTCAAT 1381
QY 1381 ATGCTTACGCTGCTGTTTGAAGATTTTACCTCCAGATCAAGTACTGATCTTAC 1440
DB 1382 ATGCTTACGCTGCTGTTTGAAGATTTTACCTCCAGATCAAGTACTGATCTTAC 1441
QY 1441 AGCAATTAATAAAGAGCGTCTCTAAACAGTCTGTAACCTTGCAGAACTC 1500
DB 1442 AGCAATTAATAAAGAGCGTCTCTAAACAGTCTGTAACCTTGCAGAACTC 1501
QY 1501 AATGTTGCTTCAATTTCTTAACTGACCTTCTGAGTGTGACAGCTTTTAC 1560
DB 1502 AATGTTGCTTCAATTTCTTAACTGACCTTCTGAGTGTGACAGCTTTTAC 1561
QY 1561 GTATGATCATTTGATCAAAATTTCAAGTTTCCACCCATGGCTGATTTCTCCAGAGCTGC 1620
DB 1562 GTATGATCATTTGATCAAAATTTCAAGTTTCCACCCATGGCTGATTTCTCCAGAGCTGC 1621
QY 1621 CAGAGATGAGGTCATATAAAGCAGGAGCAATCATTCATGTAAGTCTGAGCTAAGA 1680
DB 1622 CAGAGATGAGGTCATATAAAGCAGGAGCAATCATTCATGTAAGTCTGAGCTAAGA 1681
QY 1681 GAATTTGTCAAAAAATATAGCAAGTATCAAGTGAAGTGTATGAGGCTGAGCTGATCT 1740
DB 1682 GAATTTGTCAAAAAATATAGCAAGTATCAAGTGAAGTGTATGAGGCTGAGCTGATCT 1741
QY 1741 TATTAAGTGTGATCCCAAGAAATATAGAGAAACCACTTAAGAGATTTTCAAGTGTCT 1800
DB 1742 TATTAAGTGTGATCCCAAGAAATATAGAGAAACCACTTAAGAGATTTTCAAGTGTCT 1801
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QY	1801	GAATTAATCTGCAACATAA	CTGTGTATTCGAC	CAATCGGAGCCACA	AGCTGGTGTG	1860
Dp	1802	GAATTAATCTGCAACATAA	CTGTGTATTCGAC	CAATCGGAGCCACA	AGCTGGTGTG	1861
QY	1861	GCTGTGACTGTGACCTCC	CTGTGACTTA	CTGTGATCTG	CGCCCTGGATCTGAGATG	1920
Dp	1862	GCTGTGACTGTGACCTCC	CTGTGACTTA	CTGTGATCTG	CGCCCTGGATCTGAGATG	1921
QY	1921	TGCCAGTGGACCCAGACT	CGGCGCAGGGCC	CAGAA	CATACCTT	1980
Dp	1922	TGCCAGTGGACCCAGACT	CGGCGCAGGGCC	CAGAA	CATACCTT	1981
QY	1981	AACCTCCAGTTCAATGCT	TTATTTCATATG	TGAACATGA	TTCTGCTGGGTGAAAAGT	2040
Dp	1982	AACCTCCAGTTCAATGCT	TTATTTCATATG	TGAACATGA	TTCTGCTGGGTGAAAAGT	2041
QY	2041	GAATTTGTAACCTTA	CCCTAGAAAAA	GAATATACATG	ATTTTCTTCATGAGGAACTTT	2100
Dp	2042	GAATTTGTAACCTTA	CCCTAGAAAAA	GAATATACATG	ATTTTCTTCATGAGGAACTTT	2101
QY	2101	GTCCCTGGCAAGAGCAT	TGTG3AAAAT	ATCATCAATC	GATTTGAGAAAGTTTACAGTCC	2160
Dp	2102	GTCCCTGGCAAGAGCAT	TGTG3AAAAT	ATCATCAATC	GATTTGAGAAAGTTTACAGTCC	2161
QY	2161	ATCTTTGTTTGTCTCC	CAACTTTGTCC	AGAGTGA	GTGTGCCATTAAGAACTGATTTT	2220
Dp	2162	ATCTTTGTTTGTCTCC	CAACTTTGTCC	AGAGTGA	GTGTGCCATTAAGAACTGATTTT	2221
QY	2221	GCCCATCAACATCTCTT	TCATGAGAGATCT	TAATACTAAT	TCCTCATCTGAGAAACC	2280
Dp	2222	GCCCATCAACATCTCTT	TCATGAGAGATCT	TAATACTAAT	TCCTCATCTGAGAAACC	2281
QY	2281	ATTCCACAGAAACAGCAT	TCCCAACAGTAC	CAACAAGGCTCT	CATGACACGACG	2340
Dp	2282	ATTCCACAGAAACAGCAT	TCCCAACAGTAC	CAACAAGGCTCT	CATGACACGACG	2341
QY	2341	ACTTAATTTGCAGTGG	CCCAAGAGAAAGCA	AGTGGGCTCTTT	TGGGCTTAACATTTGA	2400
Dp	2342	ACTTAATTTGCAGTGG	CCCAAGAGAAAGCA	AGTGGGCTCTTT	TGGGCTTAACATTTGA	2401
QY	2401	GGCGCTTTAATATGA	AAATTAACA	CTGTGACTG	AAAAACATGATGAAATCTTAAAA	2460
Dp	2402	GGCGCTTTAATATGA	AAATTAACA	CTGTGACTG	AAAAACATGATGAAATCTTAAAA	2461
QY	2461	AATTTAGGAAATTCAA	ACTTAAGAAACCAT	TATTTTACTTGATGA	TGTGAATAGTACGT	2520
Dp	2462	AATTTAGGAAATTCAA	ACTTAAGAAACCAT	TATTTTACTTGATGA	TGTGAATAGTACGT	2521
QY	2521	CGTAAGTACTGTCTG	AGGTGCTCCAT	TATCTCATGCTT	CACGAAAGACTTAA	2580
Dp	2522	CGTAAGTACTGTCTG	AGGTGCTCCAT	TATCTCATGCTT	CACGAAAGACTTAA	2581
QY	2581	AAACAATCTTCACTG	GGGGAACGAGCTA	GCGGTGAGGTTAC	CGCCGCTTAAGAGAC	2640
Dp	2582	AAACAATCTTCACTG	GGGGAACGAGCTA	GCGGTGAGGTTAC	CGCCGCTTAAGAGAC	2641
QY	2641	AGCCCAAGTCTCTT	CGTATATCATATAT	TGTTCAAA	TGAAACAGTCTCTTTGAGTAA	2700
Dp	2642	AGCCCAAGTCTCTT	CGTATATCATATAT	TGTTCAAA	TGAAACAGTCTCTTTGAGTAA	2701
QY	2701	ATGCTCAGTTTTCAG	CTCTCTCCAC	CTCTGCTTCC	CAATGGAATTCGTG	2753
Dp	2702	ATGCTCAGTTTTCAG	CTCTCTCTCCAC	CTCTGCTTCC	CAATGGAATTCGTG	2754
RESULT 8						
AAS42521 standard; cDNA; 2940 BP.						
ID	AAS42521 standard; cDNA; 2940 BP.					
XX	AAS42521;					
XX	18-DEC-2001 (first entry)					

DE Human cDNA encoding an mdct protein, clone LI:007302.1:2000MWY01.

XX Human, molecules for disease detection and treatment; mdct; ss;
KW Antiarteriosclerotic; hepatotropic; antipsoriatic; cytostatic;
KW immunosuppressive; antidiabetic; antiasthmatic; neuroprotective;
KW osteoprotic; antiarthritic; cell proliferative disorder;
KW arteriosclerosis; cirrhosis; psoriasis; cancer; adenocarcinoma;
KW leukaemia; breast cancer; autoimmune disorder; AIDS;
KW acquired immunodeficiency syndrome; Addison's disease; diabetes mellitus;
KW asthma; multiple sclerosis; osteoarthritis.

XX Homo sapiens.

OS WO200162922-A2.

PN 30-AUG-2001.

PD 21-FEB-2001; 2001WO-US005896.

PF 24-FEB-2000; 2000US-0185213P.
PR 16-MAY-2000; 2000US-0205232P.
PR 17-MAY-2000; 2000US-0205285P.
PR 17-MAY-2000; 2000US-0205286P.
PR 17-MAY-2000; 2000US-0205287P.
PR 17-MAY-2000; 2000US-0205323P.
PR 17-MAY-2000; 2000US-0205324P.

XX (INCYTE GENOMICS INC.

PA Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC;
PI Chen A, D'sa SA, Amshey S, Dahl CK, Dam TC, Daniels SE, Dufour GE;
PI Flores V, Fong WT, Greenwalt LB, Hillman JL, Jones AV, Liu TF;
PI Roseberry AM, Rosen BH, Russo PB, Stockdreher TK, Daffo A;
PI Wright RJ, Yap PE, Bradley DL, Bratcher SR, Chen W;
PI Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;
XX WPI; 2001-570631/64.
XX P-PSDB; AAU25469.

XX New disease detection and treatment molecule polynucleotides and
PT polypeptides, useful for diagnosis and treatment of arteriosclerosis,
PT cirrhosis, psoriasis, cancer, autoimmune disorders, diabetes mellitus,
PT asthma and multiple sclerosis.

XX Claim 1; Page 145; 183pp; English.

XX The invention relates to novel human molecules for disease detection and
CC treatment (mdct proteins) and the polynucleotides encoding them. The MDCT
CC polynucleotides and polypeptides are useful for diagnostic and
CC therapeutic purposes e.g. to diagnose and treat cell proliferative
CC disorders (e.g. arteriosclerosis, cirrhosis and psoriasis) cancers (e.g.
CC adenocarcinoma, leukaemia and breast cancer) autoimmune disorders (e.g.
CC acquired immunodeficiency syndrome (AIDS) and Addison's disease) diabetes
CC mellitus, asthma, multiple sclerosis, osteoarthritis, and many more
CC diseases given in the specification. The present sequence encodes an mdct
CC protein of the invention

XX Sequence 2940 BP; 898 A; 596 C; 554 G; 892 T; 0 U; 0 Other;

XX

XX Query Match 99.1%; Score 2727.8; DB 5; Length 2940;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 2751; Conservative 0; Mismatches 2; Indels 2; Gaps 2

XX 1 AGAATTGGACATCATCAAGTGTCTGGAAGAAGAACACCCCTTAGATAGCACTGC 60
XX 2 AGAATTGGACATCATCAAGTGTCTGGAAGAAGAACACCCCTTAGATAGCACTGC 61

XX 61 AACATCATGACCAAGAACAAAGAACTTATTGTTAAAGCTTCATTTGTTGCCATTATG 120
XX 62 AACATCATGACCAAGAACAAAGAACTTATTGTTAAAGCTTCATTTGTTGCCATTATG 121

XX 121 ATCATATAGTTGGAAACCAAGATCACTTCTCCACGGAATGATTTGGCACTAGACAG 180

Db 122 ATCATATATGTTGGACCAAGAAATCCAGTTCTCCGACGGAAATGAATTTGCTAGTACAG 181
Qy 181 TCAAAAAGAGGCTTATTCATGTTCCAAAAGACCTACCGCTGAAAAACCAAGCTTAGAT 240
Db 182 TCAAAAAGAGGCTTATTCATGTTCCAAAAGACCTACCGCTGAAAAACCAAGCTTAGAT 241
Qy 241 ATGTCTCAGAACTACATGCTGAGCTTCAGGTCTCTGACATGAGCTTTCTATCAAGTTG 300
Db 242 ATGTCTCAGAACTACATGCTGAGCTTCAGGTCTCTGACATGAGCTTTCTATCAAGTTG 301
Qy 301 ACAGTTTGGAGCTTCCCATTAACGAATCCAGACTGATTTAGTTAGTCTTTTCAAGTTG 360
Db 302 ACAGTTTGGAGCTTCCCATTAACGAATCCAGACTGATTTAGTTAGTCTTTTCAAGTTG 361
Qy 361 AACCGAGATTGAGATTTGGATTATCTCATTAATCAGTTGCCAAAAGATCTCGCAT 420
Db 362 AACCGAGATTGAGATTTGGATTATCTCATTAATCAGTTGCCAAAAGATCTCGCAT 421
Qy 421 CCTATTTGAGCTTTCAGGCAATTTAGATCTCTCATTCATGATTTTCAAGGCTGCCCCATC 480
Db 422 CCTATTTGAGCTTTCAGGCAATTTAGATCTCTCATTCATGATTTTCAAGGCTGCCCCATC 481
Qy 481 TGTAAAGAAATTTGGCAACTTATCACAACTGAATTTCTTGGGATGAGTGTATGAAAGCTG 541
Db 482 TGTAAAGAAATTTGGCAACTTATCACAACTGAATTTCTTGGGATGAGTGTATGAAAGCTG 541
Qy 541 CAAAATATGATTTGCTGCAATTTGCTCACTTGCACTCTAAGTTATATCTTCTGAGTTTA 600
Db 542 CAAAATATGATTTGCTGCAATTTGCTCACTTGCACTCTAAGTTATATCTTCTGAGTTTA 601
Qy 601 AGAAAATTTAT 660
Db 602 AGAAAATTTAT 661
Qy 661 CTTCACCTGTTTTTCAACCACTAGTTTATTCGCTATCCAGTGAACATACAGTTAT 720
Db 662 CTTCACCTGTTTTTCAACCACTAGTTTATTCGCTATCCAGTGAACATACAGTTAT 721
Qy 721 ACTTAGGGGTGCTTCAACTGACTAAATTTAATGATGATGACAACTGTCAAGTTTC 780
Db 722 ACTTAGGGGTGCTTCAACTGACTAAATTTAATGATGATGACAACTGTCAAGTTTC 781
Qy 781 ATTAATATTTTATATCAAGAACTACACAGAGGTCAACCTTACTGAATTTTACCCTCAACAC 840
Db 782 ATTAATATTTTATATCAAGAACTACACAGAGGTCAACCTTACTGAATTTTACCCTCAACAC 841
Qy 841 ATAGAAAGCACTTGGAAATGCTGTGTGACAGTCTTTCATTTCTTTGGCCCAACCTGTG 900
Db 842 ATAGAAAGCACTTGGAAATGCTGTGTGACAGTCTTTCATTTCTTTGGCCCAACCTGTG 901
Qy 901 GAATATCTCAATATTTTCAATTTTAACTAATTTGAAAGCATTCGTGAAGAAATTTTACT 960
Db 902 GAATATCTCAATATTTTCAATTTTAACTAATTTGAAAGCATTCGTGAAGAAATTTTACT 961
Qy 961 TATTTTAAACGACATTTGAAGCATTTGACATATAGAACATATACAGAACCAAGTTTTCG 1020
Db 962 TATTTTAAACGACATTTGAAGCATTTGACATATAGAACATATACAGAACCAAGTTTTCG 1021
Qy 1021 TTTTACAGACAGCTTTGTACACCGTGTCTTCTGAGATGACATATATGATGTTAACCAT 1080
Db 1022 TTTTACAGACAGCTTTGTACACCGTGTCTTCTGAGATGACATATATGATGTTAACCAT 1081
Qy 1081 TCAGATACACCTTTTATACAGATGCTGTGTCTCATGACCAAGCAATTCAGATTTTTCG 1140
Db 1082 TCAGATACACCTTTTATACAGATGCTGTGTCTCATGACCAAGCAATTCAGATTTTTCG 1141
Qy 1141 AACCTTACCCAGAGCGTTTTCACAGATAGATTTTGGAAAAATGTTCCAGTTAGTTAA 1200
Db 1142 AACCTTACCCAGAGCGTTTTCACAGATAGATTTTGGAAAAATGTTCCAGTTAGTTAA 1201
Qy 1201 TTGGAGACACTTATCTTACAAAAAAATGATTTAAAGACTTTTCAAAGTAGTCTCATG 1260
Db 1202 TTGGAGACACTTATCTTACAAAAAAATGATTTAAAGACTTTTCAAAGTAGTCTCATG 1261

Qy 1261 ACGAAGATATGCTTCTTTTGGAAATACCTGATGTTAGCTGGAATCTTTGGAATCTGCT 1320
Db 1262 ACGAAGATATGCTTCTTTTGGAAATACCTGATGTTAGCTGGAATCTTTGGAATCTGCT 1321
Qy 1321 AGACATTAAGAAACTGCACTTTGGGTGAGATATAGTGTGTTAAATTTGTCTTCAAT 1380
Db 1322 AGACATTAAGAAACTGCACTTTGGGTGAGATATAGTGTGTTAAATTTGTCTTCAAT 1381
Qy 1381 ATGCTTACTGACTCTGTTTTGAGATGTTTACTCCTCCAGATCAAGTACTGATCTTGCAC 1440
Db 1382 ATGCTTACTGACTCTGTTTTGAGATGTTTACTCCTCCAGATCAAGTACTGATCTTGCAC 1441
Qy 1441 AGCAATTAATTAAGAGCGTTCTTAAACAAGTGTAAACTGGAAGCTTTGCAAGAACTC 1500
Db 1442 AGCAATTAATTAAGAGCGTTCTTAAACAAGTGTAAACTGGAAGCTTTGCAAGAACTC 1501
Qy 1501 AATGTTGCTTTCATCTTTTAACTGACCTTCTGGAATGTCAGCTTTTGAAGCCTTTCT 1560
Db 1502 AATGTTGCTTTCATCTTTTAACTGACCTTCTGGAATGTCAGCTTTTGAAGCCTTTCT 1561
Qy 1561 GATATGATCATTTGATCACAATTCAGTTTCCCAACCATGCGCTGATTTCTTCCAGAGCTGC 1620
Db 1562 GATATGATCATTTGATCACAATTCAGTTTCCCAACCATGCGCTGATTTCTTCCAGAGCTGC 1621
Qy 1621 CAGAAATGAGGTCAATTAAGCAAGGGGCAATCCATTCATGTTACCTGTGAGCTAAGA 1680
Db 1622 CAGAAATGAGGTCAATTAAGCAAGGGGCAATCCATTCATGTTACCTGTGAGCTAAGA 1681
Qy 1681 GAATTTGTCAAAAATATATGACCAAGTATCAAGTGAAGTGTAGAGGCTGCGCTGATCT 1740
Db 1682 GAATTTGTCAAAAATATATGACCAAGTATCAAGTGAAGTGTAGAGGCTGCGCTGATCT 1741
Qy 1741 TATAAGTGTGACTACCCAGAAAGTTATAGAGAAAGCCCACTAAAGACTTTTCACTGCT 1800
Db 1742 TATAAGTGTGACTACCCAGAAAGTTATAGAGAAAGCCCACTAAAGACTTTTCACTGCT 1801
Qy 1801 GAATATCTCTGCAACATTAATCTGTGTATGCTCAACATCGGTGCCACATGCTGTGTTG 1860
Db 1802 GAATATCTCTGCAACATTAATCTGTGTATGCTCAACATCGGTGCCACATGCTGTGTTG 1861
Qy 1861 GCTGTGACTGTGACCTCCCTCTGTGACTTATCTTGGATCTGCTGGTATCTCAGATGCTG 1920
Db 1862 GCTGTGACTGTGACCTCCCTCTGTGACTTATCTTGGATCTGCTGGTATCTCAGATGCTG 1921
Qy 1921 TGCCAGTGGAGCCGAGACTGGGGCGAGGGCCAGAAACATACCTTGAAGAACTCCAAAGA 1980
Db 1922 TGCCAGTGGAGCCGAGACTGGGGCGAGGGCCAGAAACATACCTTGAAGAACTCCAAAGA 1981
Qy 1981 AACCTCCAGTTTCAATGCTTTTATTTATATATATATATATATATATATATATATATATAT 2040
Db 1982 AACCTCCAGTTTCAATGCTTTTATTTATATATATATATATATATATATATATATATATAT 2041
Qy 2041 GAATTTGTAACCTTACCTTGAAGAAAGATATATACAGATTTGTCTTCAAGAGAACTTT 2100
Db 2042 GAATTTGTAACCTTACCTTGAAGAAAGATATATACAGATTTGTCTTCAAGAGAACTTT 2101
Qy 2101 GTCCCTGGCAAGAGATTTGTGGAATATATCACTGATTTGGAAGAGTTTCAAGTCC 2160
Db 2102 GTCCCTGGCAAGAGATTTGTGGAATATATCACTGATTTGGAAGAGTTTCAAGTCC 2161
Qy 2161 ATCTTTGTTTGTCTCCCAACTTTGTCCAGAGTGAAGTGTGCATTAAGAACTCTATTTT 2220
Db 2162 ATCTTTGTTTGTCTCCCAACTTTGTCCAGAGTGAAGTGTGCATTAAGAACTCTATTTT 2221
Qy 2221 GCCCATCAATCTCTTTCATGAGAGATCTAATACTTAATCTCTCATCTTACGGAACCC 2280
Db 2222 GCCCATCAATCTCTTTCATGAGAGATCTAATACTTAATCTCTCATCTTACGGAACCC 2281
Qy 2281 ATTCACAGAACAGATTTCCCAACAAGTACCAACAGCTGAAGGCTCTCATGACGAGCGG 2340
Db 2282 ATTCACAGAACAGATTTCCCAACAAGTACCAACAGCTGAAGGCTCTCATGACGAGCGG 2341

QY 2341 ACTTATTGTCAGTGGCCCAAGAGAAACAAACGT-GGGCTCTTTTGGGCTTAACATTAG 2399
XX |||||
Db 2342 ACTTATTGTCAGTGGCCCAAGAGAAACAAACGTGGGGCTCTTTTGGGCTTAACATTAG 2401
QY 2400 AGCCGCTTTTAAATATGAATTAACACTAGTCACTGAAACCATGATGTGAATCTTAA 2459
Db 2402 AGCCGCTTTTAAATATGAATTAACACTAGTCACTGAAACCATGATGTGAATCTTAA 2461
QY 2460 AAATTAGGAATTCAACTTAAGAAACCAATTATTTCTTGGATGATGGAATAGTACAG 2519
Db 2462 AAATTAGGAATTCAACTTAAGAAACCAATTATTTCTTGGATGATGGAATAGTACAG 2521
QY 2520 TCGTAAGTAACTGTCTGAGAGTGCCCTCACTTATCTCATGCTTCAGAAAGACTTAACA 2579
Db 2522 TCGTAAGTAACTGTCTGAGAGTGCCCTCACTTATCTCATGCTTCAGAAAGACTTAACA 2581
QY 2580 AAAACAAATTTTCACTCTGGGGAACCTGAGCTAGGCGGTGAGGTTAGCTGCCAGTTAGAGA 2639
Db 2582 AAAACAAATTTTCACTCTGGGGAACCTGAGCTAGGCGGTGAGGTTAGCTGCCAGTTAGAGA 2641
QY 2640 CAGCCAGCTCTCTGCTGTTAATCATTAATGTTTCAAAAT-GAAACAGTCTCTTTGAGT 2698
Db 2642 CAGCCAGCTCTCTGCTGTTAATCATTAATGTTTCAAAATGAAACAGTCTCTTTGAGT 2701
QY 2699 AAATCTCAGTTTTCAGCTCCTCTCCACTCTGCTTCCCAATGATTCGTG 2753
Db 2702 AAATCTCAGTTTTCAGCTCCTCTCTCCACTCTGCTTCCCAATGATTCGTG 2756

RESULT 9
ADV42616
ID ADV42616 standard; cDNA; 2391 BP.

XX ADV42616;

XX 10-MAR-2005 (first entry)

XX Human psychoneuroendocrine immune expressed sequence tag SEQ ID NO 244.

XX microarray; psychoneuroendocrine immune; chronic fatigue;

XX non-insulin dependent diabetes; allergy; immune disorder; inflammation;

XX cancer; neoplasm; infection; expressed sequence tag; ss.

OS Homo sapiens.

XX WO2004108899-A2.

XX 16-DEC-2004.

XX 04-JUN-2004; 2004WO-US017686.

XX 04-JUN-2003; 2003US-0475915P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Nicholson A, Vernon SD;

XX WPI; 2005-031682/03.

XX New microarray comprising probes for genes involved in
PT psychoneuroendocrine immune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.

XX Claim 1; SEQ ID NO 244; 254bp; English.

XX The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrine immune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CRS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrine immune gene expressed sequence tag. Note the
CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to

CC SEQ ID NO 1829 are provided.
XX
SQ Sequence 2391 BP; 742 A; 485 C; 436 G; 728 T; 0 U; 0 Other;

Query Match 86.9%; Score 2391; DB 14; Length 2391;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGACCAAGACAAAGAACCTATTTGTAAACCTTCCATTTTGTGCTTAATGATCANA 126
Db 1 ATGACCAAGACAAAGAACCTATTTGTAAACCTTCCATTTTGTGCTTAATGATCANA 60
QY 127 ATAGTTGGAACGAGAACCTAGCTTCTCCAGCGAAGAAATTTGAGTAGACAAGTCAAA 186
Db 61 ATAGTTGGAACGAGAACCTAGCTTCTCCAGCGAAGAAATTTGAGTAGACAAGTCAAA 120
QY 187 AGAGGCTTATTCATGTTCCAAAGAACCTACCGCTGAAAACCAAGTCTTAGATATGCT 246
Db 121 AGAGGCTTATTCATGTTCCAAAGAACCTACCGCTGAAAACCAAGTCTTAGATATGCT 180
QY 247 CAGAACTACATGCTGAGCTTGAAGTCTCTGACATGAGCTTTCTATCAGAGTTGACATT 306
Db 181 CAGAACTACATGCTGAGCTTGAAGTCTCTGACATGAGCTTTCTATCAGAGTTGACATT 240
QY 307 TTGAGACTTTCCTATACAGAAATCCAGCTACTGATTTAAGTGTTCGAAGTTCAACCG 366
Db 241 TTGAGACTTTCCTATACAGAAATCCAGCTACTGATTTAAGTGTTCGAAGTTCAACCG 300
QY 367 GATTTAGAAATATTTGATTTATCTCATATATCATGTCGAAAGATATCTGCATCTATT 426
Db 301 GATTTAGAAATATTTGATTTATCTCATATATCATGTCGAAAGATATCTGCATCTATT 360
QY 427 GTGAGTTTCAGGCAATTTAGATCTCTCATTCATGATTTTCAAGCCCTGCGCATCTGAG 486
Db 361 GTGAGTTTCAGGCAATTTAGATCTCTCATTCATGATTTTCAAGCCCTGCGCATCTGAG 420
QY 487 GAATTTGGCAACTTATACCACTGAATTTCTTGGGATGAGGCTATGAAAGCTGCAAAA 546
Db 421 GAATTTGGCAACTTATACCACTGAATTTCTTGGGATGAGGCTATGAAAGCTGCAAAA 480
QY 547 TTGAGTTTCTGCGCAATTTGCTCACTTGAATCTAATGATTTATCTTGTGATTTAAGAA 606
Db 481 TTGAGTTTCTGCGCAATTTGCTCACTTGAATCTAATGATTTATCTTGTGATTTAAGAA 540
QY 607 TATTTATATAAAGAAATGAGACAGAAAGTCTACAAATTTGCAATGCAAAAACCTTCA 666
Db 541 TATTTATATAAAGAAATGAGACAGAAAGTCTACAAATTTGCAATGCAAAAACCTTCA 600
QY 667 CTGTTTTCACCCAACTAGTTTATTTGGCTATCCAGGAACATATCGTTAATCTTTA 726
Db 601 CTGTTTTCACCCAACTAGTTTATTTGGCTATCCAGGAACATATCGTTAATCTTTA 660
QY 727 GGGTCTTACAACTGACTAATTAATTAATTTGAATGATGACAACTGCAAGTTTCAATTA 786
Db 661 GGGTCTTACAACTGACTAATTAATTAATTTGAATGATGACAACTGCAAGTTTCAATTA 720
QY 787 TTTTATATGAACTACCAAGAGTTCAACTTACTGAATTTTACCTCAACCAATAGAA 846
Db 721 TTTTATATGAACTACCAAGAGTTCAACTTACTGAATTTTACCTCAACCAATAGAA 780
QY 847 ACGACTTGAAGATGCTGGTCAAGAGTCTTCAATTTCTTGGCCCAACCTGTGAATAT 906
Db 781 ACGACTTGAAGATGCTGGTCAAGAGTCTTCAATTTCTTGGCCCAACCTGTGAATAT 840
QY 907 CTCATATTTTCAATTTTACAAATTAATTTGAAGCATTCGTGAAGAAATTTTACTATTCT 966
Db 841 CTCATATTTTCAATTTTACAAATTAATTTGAAGCATTCGTGAAGAAATTTTACTATTCT 900
QY 967 AAAAGCAATGGAAGCATTTGACATATGACAAATATCAGAAACCAAGTTTCTGTTTCA 1026
Db 901 AAAAGCAATGGAAGCATTTGACATATGACAAATATCAGAAACCAAGTTTCTGTTTCA 960
QY 1027 CAGACAGCTTTGTACACCGTGTCTTGTGAGATGAACATTAATGATGTTAACCATTTCA 1086

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Db      |||
361     CAGACAGCTTGTGACCGTGTGTTCTGAGATGAAATATGATGATTAACATTTCAAGT 1020
Qy      1087  ACACCTTTTATACAAATGCTGTGCTCAATGCAACAGACATTAAGTTTGAACCTT 1146
Db      1021  ACACCTTTTATACAAATGCTGTGCTCAATGCAACAGACATTAAGTTTGAACCTT 1080
Qy      1147  ACCCGAAGCTTTTACAGATAGTATTTTGGAAAAATGTTCCACGTTAGTTAAATTTGAG 1206
Db      1081  ACCCGAAGCTTTTACAGATAGTATTTTGGAAAAATGTTCCACGTTAGTTAAATTTGAG 1140
Qy      1207  ACACCTTTTATACAAATGCTGTGCTCAATGCAACAGACATTAAGTTTGAACCTT 1266
Db      1141  ACACCTTTTATACAAATGCTGTGCTCAATGCAACAGACATTAAGTTTGAACCTT 1200
Qy      1267  GATATGCTCTCTTTGGAAAAATGCTGATGTTAGCTGAAATCTTTGGAAATCTGGTGAACAT 1326
Db      1201  GATATGCTCTCTTTGGAAAAATGCTGATGTTAGCTGAAATCTTTGGAAATCTGGTGAACAT 1260
Qy      1327  AAAGAAAACCTGACCTTGGGTTGAGAGTATAGTGTGTTAAATTTGCTTCAATATGCTT 1386
Db      1281  AAAGAAAACCTGACCTTGGGTTGAGAGTATAGTGTGTTAAATTTGCTTCAATATGCTT 1320
Qy      1387  ACTGACTCTGTTTCAAGATGTTTAACTCTCCAGATCAAGGTAATTGATCTTCAACAGCAAT 1446
Db      1321  ACTGACTCTGTTTCAAGATGTTTAACTCTCCAGATCAAGGTAATTGATCTTCAACAGCAAT 1380
Qy      1447  AAAATAAAGAGCGTTCCTAAACAAGTCGTAACCTGGAAAGCTTTCGAACAACTCAATGTT 1506
Db      1381  AAAATAAAGAGCGTTCCTAAACAAGTCGTAACCTGGAAAGCTTTCGAACAACTCAATGTT 1440
Qy      1507  GCTTTCATTTCTTTAACTGACCTTCTCGATGTGGAGCTTTTAAAGACCTTCTGTATTTG 1566
Db      1441  GCTTTCATTTCTTTAACTGACCTTCTCGATGTGGAGCTTTTAAAGACCTTCTGTATTTG 1500
Qy      1567  ATCATTGATCACAATTCAGTTTCCCAACCCATGCGCTGATTTCTTCCAGAGCTGCCAAG 1626
Db      1501  ATCATTGATCACAATTCAGTTTCCCAACCCATGCGCTGATTTCTTCCAGAGCTGCCAAG 1560
Qy      1627  ATGAGTCAATTAAGAGCGGGGCAATCAGTCCAAATGTAACCTGGAGCTAAGAGAAATTT 1686
Db      1561  ATGAGTCAATTAAGAGCGGGGCAATCAGTCCAAATGTAACCTGGAGCTAAGAGAAATTT 1620
Qy      1687  GTCAAAAATATAGACCAAGTATCAAGTAAAGTGTATAGAGGCTGCGCTGATCTTATTAAG 1746
Db      1621  GTCAAAAATATAGACCAAGTATCAAGTAAAGTGTATAGAGGCTGCGCTGATCTTATTAAG 1680
Qy      1747  TGTGACTACCCAGAAAGTTATAGAGAGCCCACTAAGACCTTTCACATGCTGAAATTA 1806
Db      1681  TGTGACTACCCAGAAAGTTATAGAGAGCCCACTAAGACCTTTCACATGCTGAAATTA 1740
Qy      1807  TCCCTCAACATTAACCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1866
Db      1741  TCCCTCAACATTAACCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1800
Qy      1867  ACTGTGACCTCCCTGTGACATCTTATGATGCTGCTGCTGATCTCAGATGCTGCTGAG 1926
Db      1801  ACTGTGACCTCCCTGTGACATCTTATGATGCTGCTGCTGCTGATCTCAGATGCTGCTGAG 1860
Qy      1927  TGGACCCAGACTGCGGCGCAGGCGCAAGACATACCTTGAAGAACTCCAAAGAAACCTC 1986
Db      1861  TGGACCCAGACTGCGGCGCAGGCGCAAGACATACCTTGAAGAACTCCAAAGAAACCTC 1920
Qy      1987  CAGTTTCATGCTTTTATTTATATAGTGAACATGATCTGCGCTGGGTGAAAAAGTGAATTG 2046
Db      1921  CAGTTTCATGCTTTTATTTATATAGTGAACATGATCTGCGCTGGGTGAAAAAGTGAATTG 1980
Qy      2047  GTACCTTACCTAGAAAAAGAGATATACAGATTTGTCTTCAATGAGAGAACTTTGTCCCT 2106
Db      1981  GTACCTTACCTAGAAAAAGAGATATACAGATTTGTCTTCAATGAGAGAACTTTGTCCCT 2040
Qy      2107  GGCAGAGCATTTGTGAAAAATATCATCAATGCAATGAGAGATTTCAAGTCCATCTTT 2166

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Db      2041  GGCAGAGCATTTGTGAAAAATATCATCAATGCAATGAGAGATTTACAGATCCATCTTT 2100
Qy      2167  GTTTTGTCTCCCAACTTTGTCCAGAGTGAAGTGTCCTTATACGAATCTATTTGGCCAT 2226
Db      2101  GTTTTGTCTCCCAACTTTGTCCAGAGTGAAGTGTCCTTATACGAATCTATTTGGCCAT 2160
Qy      2227  CACAATCTCTTTCAATGAAGATCTTAATTAATCTCTATCTTATCTGGAACCAATTTCCA 2286
Db      2161  CACAATCTCTTTCAATGAAGATCTTAATTAATCTCTATCTTATCTGGAACCAATTTCCA 2220
Qy      2287  CAGAACAGACATTTCCCAACATACCAAGCTGAAGGCTCCATGAGCAGCGGACTTAT 2346
Db      2221  CAGAACAGACATTTCCCAACATACCAAGCTGAAGGCTCCATGAGCAGCGGACTTAT 2280
Qy      2347  TTGCACTGCGCCCAAGAGAAAGCAACGTCGCTCTTTTGGGCTAAACATTAAGCCGCT 2406
Db      2281  TTGCACTGCGCCCAAGAGAAAGCAACGTCGCTCTTTTGGGCTAAACATTAAGCCGCT 2340
Qy      2407  TTTAATATGAATTTAACAATGCTACCTGAAAAACAATGATGGAATCTTAA 2457
Db      2341  TTTAATATGAATTTAACAATGCTACCTGAAAAACAATGATGGAATCTTAA 2391

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RESULT 10

AAA39810
ID AAA39810 standard; cDNA; 2604 BP.

AAA39810;
AC AC
XX XX
DT 22-SEP-2000 (first entry)

XX Murine Toll-like receptor TLR6 cDNA.

XX Toll-like receptor; TLR6; murine; anti-infectious; treatment; infection;
XX transcription factor; NF-kappaB; immune response; ss.

XX Mus sp.

XX Key Location/Qualifiers
FH 21.2442
FT /tag=a
FT /product="TLR6"

XX WO20024776-A1.

XX PD 04-MAY-2000.

XX PF 26-OCT-1999; 99WO-JP005917.

XX PR 26-OCT-1998; 98JP-00304110.

XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX PI Akira S, Takeuchi O;

XX DR WPI; 2000-350697/30.

XX DR P-PSDB; AAY88055.

XX PT Toll-like receptor TLR6 molecule and encoded gene, participating in
XX signal transduction of initial immune response, applicable e.g. in
XX treating infections.

XX PS Claim 4; Page 29-30; 35pp; Japanese.

XX This invention describes a novel toll-like receptor TLR6 which has
XX anti-infectious activity. The protein and its encoded gene have clinical
XX use e.g. in treating infections. Toll family receptors are related to
XX transcription factor NF-kappaB and regulate the expression of various
XX genes participating in the immune response. This sequence encodes the
XX murine TLR6 protein which is described in the method of the invention
XX
XX Sequence 2604 BP; 689 A; 615 C; 561 G; 739 T; 0 U; 0 Other;

Query Match 55.7%; Score 1533.6; DB 3; Length 2604;
 Best Local Similarity 76.1%; Pred. No. 0;
 Matches 1990; Conservative 0; Mismatches 596; Indels 10; Gaps 3;

17 TCAAGATGCTTGAAGAAGAACAAACCTTTAGATAGCCATCATGACCAAG 76
 4 TAAAAATGCTGAGAAATGTAATGTCCTCTGGATAGCCTCTCAACATGACCAAG 63

77 ACAAAAGACCTATGTTAAAGCTTCATTTGTTGGCTTATGATCATATAGTTGAA 136
 64 ACGAAAGAACCCATCGGGAGATTTCACCTGTGTCGCCCTGAAATAGTGGA 123

137 CCGAATCCAGTCTCTCCGACGGAATGAATTTGCAGTACGACGACAAAGAGCTCTTA 196
 124 GCAATGCCCTTCTCTAATGAATTTGAGTCTATGATGATCTTCAACAGAACTTAA 183

197 TTCAATGTTCCAAAAGACCTACCGCTGAAAACCAAGCTTATATGCTCAGAACTACA 256
 184 CTCATGTCCTCCAAAGACCTGCCCAAGAACAAAGCCCTGAGTCTGTCTCAAACTCTTA 243

257 TGGCTGAGCTTCAAGCTCTGACATGAGCTTTCTATCAGATGACAGTTTGAAGCTTT 316
 244 TATCTGAGCTTGGAGTCTGATATCAGCTTCTGTGACAGAGCTGAGAGTTCTGAGACT 303

317 CCCATPAACGAATCCAGCTACTGATTTATAGTCTTCAAGTTCAACGAGATTTGAAT 376
 304 CCCAACACGAGATACGAGAGCTTGAATTTCAATGATTTCTTGTTCATACGAGACTTGAAT 363

377 ATTGGATTTATCTCATTAATCAAGTTGCAAAAGATATCTGCCATCTTATGAGTTTGA 436
 364 ACCTGGATGTCACACAAATCGGTTGCAAAACATCTTGTGCTGCCCTATGGGAGCTGA 423

437 GGCATTTAGATCTCTCATTAATGATTTCAAGGCTTCCCATCTTAAAGAAATTTGGA 496
 424 GGCATCTACACCTCTCATTAATGATTTGATGATCTGCTGTGTGAAGAAATTTGGA 483

497 ACTTATCAACATGATTTCTTGGGATGAGTGTATGAGCTGAAAGCTGCAAAATATGATTC 556
 484 ACTCAACGAGCTGACTTCTCTGAGATGAGTGTAGTGTCCAAAGTTCCGACAACTGAGTCTGC 543

557 TGGCAATGCTCACTTGCATCTTAAGTTATATCTTCTGATTTAAAGAAATTTATATA 616
 544 TCCAGTGTCTCACTTGCATCTTAAGTGTATCTTCTGACCTTAAGATCATCATATA 603

617 AAGAAATGAGCAGAAAGTCTTCAAAATTTCTGAATGCAAAAACCTTCACTTGTCTTC 676
 604 AAGGCGGGAAACGAAAGTCTTCAAGATTTCCCAATCCACCGTCTCCATTTGGTCTTC 663

677 ACCCACTAGTTTATCTGCTATCCAAAGTACATATCAGTTAATCTTAGGCTGTAC 736
 664 ATCCAAATGCTTGTCTGTCTGTAAGTAAATGCTGTAAACGCTTTAGACATTTAC 723

737 AACTGACTATATTAATTAATGAATGATGACACTGTCAAGTTTCAATTAATTTTATACG 796
 724 AACTAGTATATTAATTAATGAATGAAACCTGTCAAGGTTAATGACATTTTATACG 783

797 AACTACACGAGGTTCAACCTTACTGAATTTTACCTCAACACATAGAAACGACTTGA 856
 784 AACTACACGAGGTTCAACCTTACTGAATTTTACCTCAACACATAGAAACACCTTGA 843

857 AATGCTGGTCAAGCTTCTCAATTTCTTGGCCCAACCTGTGAATCTTCAATATTT 916
 844 AATGCTGGTCAAGCTTCTCAATTTCTTGGCCCAACCTGTGAATCTTCAATATTT 903

917 ACAATTTAACAATTAATGAAGCATTCGTGAAGAAAGATTTTACTTATTAACGACAT 976
 904 ACAATTTAACAATTAATGAAGCATTCGTGAAGAAAGATTTTACTTATCTGAGACAGCAC 963

977 TGAAGAGCTTGAATGAAATATCAAGAACCAAGTTTCTGTGTTTACAGACAGCTT 1036
 964 TGAAGAGCTTGAATGAAATATCAAGAACCAAGTTTCTGTGTTTACAGACAGCTT 1023

1037 TGTACACGCTGTGTTCTGATGAAACATATGATGTTAACATTTCAATACCTTTTA 1096

1024 TATACCTGGTGTGTTGCTGATGAGAACATCAATGTCTCTATCTCAGACACCTTTTCA 1083
 1097 TACACATGCTGTGTCTCATTCGACCAAGACATTCAGATTTTGAACCTTACCAGACG 1156
 1084 TCCACATGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1143

1157 TTTTACAGATGATATTTTGAAGAAATGTTTCAACCTTAAATTTGAGACATTAATCT 1216
 1144 TTTTATCTACAGTGTGTTTCAAGGCTGTTTCAACCTTAAAGATTTGACACATTAATCT 1203

1217 TACAAAAAATGATTTAAAGACCTTTTCAAGTATGCTCATGACGAAGATATGCTT 1276
 1204 TACAAAGATGATTTGAAGAACTTTTAAAGTATGCTCATGACGAAGATATGCTT 1263

1277 CTTTGAATTAATGATGATTTAGCTGAATCTTTTGAATCTGTGATACATTAAGAAACT 1336
 1264 CTCTGGAACCTTTGATGATTTAGTGAATCTTTTGAATCTGTGATGATGACAGACAT 1323

1337 GCACTTGGTGAAGATATAGTGTATTAATTTGCTTCAATATGCTTACTGACTG 1396
 1324 GGGCTGGGCTGAGACATATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1383

1397 TTTTCAAGATGTTTAACTCCAGATCAAGGATCTTGAATCTTCAACAGCAATTAATTAAGA 1456
 1384 TCTTCAAGATGTTTAACTCCAGATCAAGGATCTTGAATCTTCAACAGCAATTAATTAAGA 1443

1457 GGGTCTTAAACAGTGTGTAATCTGAAAGCTTTTCAAGATCTTCAATGATTTGCTTCAAT 1516
 1444 GATCCCTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1503

1517 CTTTAACTGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1576
 1504 CTTTAACTGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1563

1577 ACAATTCAGTTTCCCAACCATCGGCTGATTTCTTCAAGAGCTGCCAAGATGAGGTCAA 1636
 1564 ATTAATCTGATTTCCCAACCATCGGCTGATTTCTTCAAGAGCTGCCAAGATGAGGTCAA 1623

1637 TAAAGACAGGGGACATTCATTCATATGATCTGTGAGCTTAAGAAATTTGCAAAATA 1696
 1624 TAAAGACAGGGGACATTCATTCATATGATCTGTGAGCTTAAGAAATTTGCAAAATA 1683

1697 TAGACCAAGTATCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1756
 1684 TAGGCTGGTGAAGAAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1743

1757 CAGAAATTAATGAGAAAGCCCACTAAAGAACTTTTCAACATGCTGAATTAATCTGCAACA 1816
 1744 CAGAAATTAATGAGAAAGCCCACTAAAGAACTTTTCAACATGCTGAATTAATCTGCAACA 1803

1817 TAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1876
 1804 CTGTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1863

1877 CCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1936
 1864 TCCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1923

1937 CTGGGCGAGGGGCGAGAAATACCTTAAAGAACTCCAAAGAAACCTCCAGTTTCAATG 1996
 1924 CCGAGCAAGGGGCGAGGACATCCCTTAAGAACTCCAAAGAAACCTCCAGTTTCAATG 1983

1997 CTTTATTTTCAATATGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 2056
 1984 CTTTGTCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2043

2057 TAGAAAGAGATATTAAGATTTGCTTCAATGAGAACTTTTCTCCCTGGCAAGACA 2116
 2044 TAGAAAGAGATATTAAGATTTGCTTCAATGAGAACTTTTCTCCCTGGCAAGACA 2103

2117 TGTGAAATTAATCATCAATGATGAGAAAGATTTAAGAGTCAATCTTTGTGCTC 2176

QY 977 TGAAGCATTTGACAAATAGACATATCCAGAACAAAGTTTCTGTTTTCACAGACGCTT 1036
 Db 964 TGAAGCATTTGACAAATAGACATATCCAGAACAAAGTTTCTGTTTTCACAGACGCTT 1023
 QY 1037 TGTACACCGTGTGTTTCTGAGTGAACATTTATGTTAAACATTTGACATACCTTTTA 1096
 Db 1024 TATACTCGGTGTTTGTGAGTGAACATGATGCTCTATCTCAGACACCCCTTTTCA 1083
 QY 1097 TACACATGCTGTGCTCTCATGACCAAGACATTCAGTTTGTGAACCTTACCCAGAAG 1156
 Db 1084 TCCACATGCTGTGCTCTCATGACCAAGACATTCAGTTTGTGAACCTTACCCAGAAG 1143
 QY 1157 TTTTACAGATAGTATTTTGAAGAAATGTTCCACGTTAGTAAATGAGACATTAATCT 1216
 Db 1144 TTTTACTGACAGTGTGTTTTCAGAGCTGTTCCACCTTAAGAGATTGACAGACATTAATCT 1203
 QY 1217 TACAAAAAATGATTTAAAAAGCTTTTCAAGTAGTCTCATGACGAAGATATGCTT 1276
 Db 1204 TACAAAAAATGATTTAAAAAGCTTTTCAAGTAGTCTCATGACGAAGATATGCTT 1263
 QY 1277 CTTTGAAGAAATACGATGTTTACTGGAATCTTTGGAATCTGTGATGACATTAAGAAAAT 1336
 Db 1264 CTTGGAAGAAATGATGTTTGAATCTTTGAATCTGTGATGACATTAAGAAAAT 1323
 QY 1337 GCACTTGGGTGAGAGTATAGTGTAAATTTGCTTCAATATGCTTACTGACTCTG 1396
 Db 1324 GCGCTGGGTGAGAGCATATGTTGTTGAATTTGCTTCAATATGCTTACTGACTCTG 1383
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 Db 1384 TCTTCAATGTTTACCTCCAGAGATCAAGTATCTTGATCTTCAAGCAATTAATTAAGA 1443
 QY 1457 GCGTCCCTAAACAAATGCTAAACCTGGAAGCTTTGCAAGAACTCAATGTTCTTCAAT 1516
 Db 1444 GCATCCCTAAAGATGCTAAACCTGGAAGCTTTGCAAGAACTCAATGTTCTTCAAT 1503
 QY 1517 CTTTACTGACCTTCTGATGTTGGAGCTTTAGAGACCTTCTGATGATCAATGATC 1576
 Db 1504 CTTTACTGACCTTCTGATGTTGGAGCTTTAGAGACCTTCTGATGATCAATGATC 1563
 QY 1577 ACAATTCAGTTTCCACCCATGAGCTGATTTCTTCAAGAGCTGCCAGAGATGAGGTCA 1636
 Db 1564 ATAACTCAGTTTCCACCCATGAGCTGATTTCTTCAAGAGCTGCCAGAGATGAGGTCA 1623
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 Db 1624 TAAAGAGCGGAGCAATCCATTCATGTTACTGTTGAGCTTAAGAGATTTGTCAAAATA 1683
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 Db 1684 TAGGCTGGGTGCAAGAGAGTGGTGAAGGCTGGCTGATCTTATAAGTGTGACTACC 1743
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 Db 1744 CAGAAAGCTTAAAGAGACTGACATGAGGACTTTCACATGTTCTGATTAATTAATCTGCAACA 1803
 QY 1817 TAACTGTGCTGATCTCATCATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1876
 Db 1804 CTGTTCTGTGCTGATCTCATCATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1863
 QY 1877 CCGTCTGATCTACTGATGCTGCTGCTGATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1936
 Db 1864 TCCCTGTGCTACTGATGCTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1923
 QY 1937 CTCGCGGAGGCGCAGAGACATACCTTAAGAACTCCAAAGAAACCTCCAGTTTCAATG 1996
 Db 1924 CCAGGCAAGGCGCAGGACATCCCTTAAGAGAACTCCAGAGAAACCTCCAGTTTCAATG 1983
 QY 1997 CTTTATTTTCAATATGTAACATGATTTCTGCTGGGTGAAAGTGAATTTGTAATCTTACC 2056
 Db 1984 CTTTGTCTCAATACGTAAGCAATGATTTCTGCTGGGTGAAAGTGAATTTGTAATCTTACC 2043
 QY 2057 TAGAAAAAGATATACAGATTTGTTCTTATGAGAGAACTTGTCCCTGGCAAGAGA 2116

Db 2044 TAGAGAAAGATGACATCCGGGTTTGCTTCATGAGAGAACTTTGTCCCTGGCAAGAGA 2103
 QY 2117 TTTGTGAAATATTCATCAACTGCACTTGTGAGAGAGTTTCAAGTCCATCTTTGTTGTCTC 2176
 Db 2104 TTTGTGAGAAATTCATCAATTTTCAATGAGAGAGTTTCAAGTCCATCTTTGTTGTCTC 2163
 QY 2177 CCAACTTGTTCAGAGTGAAGTGTGCTCATTAAGAACTGATTTGTGCTGCAATCTCT 2236
 Db 2164 CCAACTTGTTCAGAGTGAAGTGTGCTCATTAAGAACTGATTTGTGCTGCAATCTCT 2223
 QY 2237 TTTCAAGAGATCTAATTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCT 2296
 Db 2224 TCCATGAGAGGCTCTGATTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCT 2283
 QY 2297 TTTCCCAAGAGTGAAGTGTGCTCATTAAGAACTGATTTGTGCTGCAATCTCT 2356
 Db 2284 TTTCCCAAGAGTGAAGTGTGCTCATTAAGAACTGATTTGTGCTGCAATCTCT 2343
 QY 2357 CCAAGGAGAGAAAGCAAGTGGGCTTTTGGGCTTAACATTTAGAGCCGCTTTTATATGA 2416
 Db 2344 CTAAGAGAGGCAAGGCTGGGCTTTTGGGCTTAACATTTAGAGCCGCTTTTATATGA 2403
 QY 2417 AATTAACTAGTCACTGAAACCAATGATGTAATCTTAAATTAATTAATTAATTAATTAATTAATTAAT 2476
 Db 2404 AGTTAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2456
 QY 2477 CTTAAGAAACATTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2536
 Db 2457 CTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2513
 QY 2537 GAGGTGCTTCATTAAT 2552
 Db 2514 GAGGTGCTTCATTAAT 2529

RESULT 12
 ADU23192
 ID ADU23192 standard; cDNA; 2604 BP.
 XX
 AC ADU23192;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE Murine Toll-like receptor 6 (TLR6) cDNA sequence - SEQ ID 84.
 XX
 screening; Toll-like receptor agonist; TLR agonist; gene; ss; TLR6.
 XX
 OS Mus sp.
 XX
 PN W02004094671-A2.
 XX
 PD 04-NOV-2004.
 XX
 PR 22-APR-2004; 2004WO-US012788.
 XX
 PR 22-APR-2003; 2003US-0464586P.
 XX
 PR 22-APR-2003; 2003US-0464586P.
 XX
 PA (COLE-) COLEY PHARM GMBH.
 XX
 PA (COLE-) COLEY PHARM GROUP INC.
 XX
 PI Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
 DR WPI, 2004-795573/78.
 XX
 PT Identifying agonists of Toll-like receptor (TLR) signaling activity.
 PT Useful therapeutically or prophylactically, comprises contacting an
 PT RPM18226 cell that expresses a TLR with a test compound and measuring TLR
 PT signaling activity.
 XX
 PS Disclosure; SEQ ID NO 84; 342pp; English.
 XX

CC The invention comprises a screening method for identifying agonists of
CC Toll-like receptor (TLR) signalling activity. The method involves
CC contacting an RPMI8226 cell (that expresses a TLR) with a test compound,
CC and measuring a test level of TLR signalling activity, where a test level
CC that is positive is indicative of a test compound that is a TLR agonist.
CC The method of the invention is useful for identifying agonists of TLR.
CC The present nucleic acid represents a TLR cDNA sequence.

XX Sequence 2604 BP; 689 A; 615 C; 561 G; 739 T; 0 U; 0 Other;

Query Match 55.7%; Score 1533.6; DB 13; Length 2604;

Best Local Similarity 76.1%; Pred. No. 0;

Matches 1930; Conservative 0; Mismatches 596; Indels 10; Gaps 3;

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Db 4 TAAAAATGCTGGAAGATGTAAGTCCCTCTGGATAGCCTCTGCACATGAGCCAA 63
Qy 77 ACAAGAACTATTTGTTAAAGCTTCATTTTGTGGCTTATGATCATATATGTTGAA 136
Db 64 ACAGAAACCCATCGTGGGAGTTTCCACTTTGTTGGCCCTGGCCTTAATATGCGAA 123
Qy 137 CCAGATTCAGTCTTCCAGCGAATGATTTGCAGTAGACAAGTCAAAAGAGCTTTA 196
Db 124 GCATGACCCCGTCTCTATGAACTTGAGTCTAGGTAGACTTATTCAAACAGAACTTA 183
Qy 197 TTCATGTTCCAAAAGACCTACCGCTGAACCAAGCTTATGATATGTCAGAACTACA 256
Db 184 CTCATGTCCCAAAACCTGCGCAACAGAAACAAAGCCTGAGTCTGTCTCAAACTCTA 243
Qy 257 TCGCTGAGCTTCAAGTCTCTGACATGAGCTTTCTATCAGAGTTGACAGTTTGAACCTT 316
Db 244 TATCTGACCTTCGAGTGCCTGATATCAGCTTCTGTGACAGCTGAGAGTTCTGACACTCT 303
Qy 317 CCCATTAAGATCCAGCTACTGATTTTAAGTCTTCAAGTTCAACCGAGATTTAGAT 376
Db 304 CCCAAAGAGATGAGGACCTTGATTTCCATGATTTCTTTGTTCAATCGAGACTTAGAT 363
Qy 377 ATTTGATTTATCTCATATACAGTTGCAAAAGATATCTGACCATCTATTTGAGATTTCA 436
Db 364 ACCTGAGTGTCTCAACATGCTGTTGCAAAACATCTCTTGCTGCCCTTATGAGGAGCTGA 423
Qy 437 GGCATTTTGAATCTCATTCATTAATGATTTCAAGGCCCTGCGCATCTGTAAAGAAATTTGCA 496
Db 424 GGCATCTGACCTCTCATTCATTAATGATTTCAAGTGTACTGCTGTGTAGTAAGAAATTTGCA 483
Qy 497 ACTTATCAACAATGAAATTTCTGGATGATGAGTCTATGAAAGTGCAGAAATTAAGATTGC 556
Db 484 ACCTGACGAAAGCTGACTTTCCTGGATTAAGTGTGCGCAAGTTCGACAACTGAGATCTGC 543
Qy 557 TGCCATTTGCTCACTTGATCATTAAGTTATCTTCTGATTTTAAGAAATTTATATATA 616
Db 544 TCCCGATGCTCACTTGATCTTAAGTGAATCTTCTGACCTTAAGTGAATCTTAATA 603
Qy 617 AAGAAATGAGACAGAAAGCTTACAAATTTCTGAATGCAAAAACCTTCACTTGTGTTTC 676
Db 604 AAGGGGGGAAACAGAAAGCTTCAAGATTCACAAATACACCGTTCTCCATTGGTCTTTC 663
Qy 677 ACCCAATAGTTATTTGCTATCCAAAGTAAACATATCAATTAATCTTAAGGTGCTTAC 736
Db 664 ATCCAAATAGCTGTTCTCTGTGTTCAAGTAAACATATGTTAAACGTTTAAAGCAATTAAC 723
Qy 737 AACTGACTATATTAATTAATGATGACAACTGTCAAGTTTTCATTAATTTTATACG 796
Db 724 AACTGATATATTAATTAATGATGACAACTGTCAAGTTTTCATTAATTTTATACG 783
Qy 797 AACTGACCAAGGTTCAACCTTATAGAAATTTTAAACCTTCAACCAATAGAAACGACTTGA 856
Db 784 AACTCACCAGAGGTCCAACTTATGAAATGACCTCCAGACAAATAGAAACAACTGGA 843
Qy 857 AATGCTGCTGAGAGCTTTTCAATTTCTTTGGCCCAACCTGTGGAATATCTCAATATTT 916
Db 844 AGTGTCTGGTTAACTTTTCAATTTCTTTGGCCCGACCGGTGAGTACTCAATATTT 903
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917 ACAATTTAACAATATTTGAAGCATTCCTGGAAGAGATTTTACTTATTTTAAAGCAT 976
Db 904 ACAATTTAACAATATTTGAAGCATTCAGAGAAATTCAGAGAGAAATTTACTTACTCGAGACAGAC 963
Qy 977 TGAAGGCTTGAACATTAAGAAATATACAGAACCAAGTTTCTGTGTTTCAAGACAGCTT 1036
Db 964 TGAAGTCACTGATGATTAAGACCGTCAAAACCAAGTGTCTCTTTTCAAGAGAGCGC 1023
Qy 1037 TGATACACCGTGTGTTTCTGAGATGAACATTAATGATTTACCATTTACATACACTTTTA 1096
Db 1024 TATCTCGGTGTGTTGCTGATGATGAACATCAAGATGCTCTATCTCAACACCCCTTTCA 1083
Qy 1097 TACACATGCTGTGCTTCATGACCAACAGACATTCAGATTTTGAACCTTAAACCAAGAG 1156
Db 1084 TCCACATGCTGTGCCCCGATCCCAAGCTCATTTTACATTTTCAAGTTTACCCAGATG 1143
Qy 1157 TTTTCAAGATATATTTTGAAGAAATGTTCCAGCTTATGTTAANTGAGACACTTATCT 1216
Db 1144 TTTTATCTGACAGTGTGTTTCAAGCTGTTCACCTTAAAGATGAGACACTTATCT 1203
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Db 1264 CTCTGAAACTTTGATGTTATGTTGAATTCCTTGAACCTCATGACATATGACAGAGAT 1323
Qy 1337 GCATTTGGTGTGAGATATAGTGTGTTAATTTGCTTCAAAATATGCTTATCTGACTG 1396
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Db 1384 TCTTATGATGCTTACTCTCCAGATCAAGTATGCTTCAAGACATTAATAAGA 1443
Qy 1457 GCGTTCCTTAAACAAGTCTTAAACCTGAAAGCTTTGCAAGAACTCAATGTTGCTTCAAT 1516
Db 1444 GCATCCATAAGATGTCACCAACCTGAGGCTTTGCAAGAACTCAATGATGATCAACT 1503
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Db 1504 CTTTATCTGACCTTCTGATGATGAGCTTTAGAGCTTTTGTATTTGATCATTTGATC 1563
Qy 1577 ACAATTTGATTTCCACCATCGGCTGATTTCTTCAAGCTGCCAGAAAGTGAAGTCAA 1636
Db 1564 ATACTCTGATTTCCATCTCTGAGATTTCTTCAAGCTGTGAGAAATTAAGATCC 1623
Qy 1637 TAAAGCAGGGGACAAATCATTCOAATGTACCTGTAGCTTAAGAAATTTGTCAAAATA 1696
Db 1624 TAAAGCGGGAACAAACCATTCOAATGTACATGTAGCTGAGGGACTTTGTCAAGAAACA 1683
Qy 1697 TAGACCAAGTATCAAGTGAATGTTAAGGGCTGTGCTGATTTCTTAATAGTGTACTAC 1756
Db 1684 TAGGCTGGGTGACAAAGAAAGTGTGAGGGCTGTGCTGATCTTCAAGTGTGACTACC 1743
Qy 1757 CAGAAAGTTATAGAGAAAGCCCACTAAGGACTTTCACATGTCTGAATTTATCTTCAACA 1816
Db 1744 CAGAAAGCTTAAGGAACTGACCTGAGGACTTTCACATGTCTGACCTGTCTGTATTA 1803
Qy 1817 TAACTCTGATATGCTCACTATGCTGTCACCATGTCATGCTGTGTGCTGTGACTGACCT 1876
Db 1804 CTGTTCTGCTGATGCTGTCACCATGCGGGGACCTATCTGCTGTGCTGTGCTGTGCTG 1863
Qy 1877 CCTCTGATCTACTTGGATCTGCTCTGTATCTCAAGATGCTGTGCTCAAGTGTGACCCGA 1936
Db 1864 TCCCTGTCTCTTACTTGAACCTGCTGTGTATGAGAGATGCTGTGTAGTGAACACGA 1923
Qy 1937 CTGCGGACAGGGCCAGAAACATACCTTAGAAGAACTCCAAGAAACCTCCAGTTTCAAG 1996
Db 1924 CCAGGACAGGGCCAGGACATCCCTTGAAGAACTCAAGAAACCTCCAGTTTCAAG 1983
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OY 1997 CTTTATTTTCATATAGTGAACATGATTTCTGCTGGGTGAAAGTGAATTGTACTTACC 2056
 DB 1984 CTTTGTGCTATACAGTGAAGCATGATTTGCTGGGTGAAGAACGAACTTACTACCAACC 2043
 OY 2057 TAGAAAAAGAAATATACAGATTTTGTCTTCATGAGAGAACTTTGCTCCGCAAGAGA 2116
 DB 2044 TAGAAGAAAGATACATCCGGGTTTGTCTCCATGAGAGAACTTTGCTCCGCAAGAGA 2103
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 DB 2164 CCACTTATTCAGAGTGAAGTGTGCTCATTAAGAACTCTATTTTGGCCATCAAACTCT 2223
 OY 2237 TTCTATGAAGATCTTAATTAATCTTATCTCATCTTACTGGAACCCATTCCAGAACAGCA 2296
 DB 2224 TCCATGAAGGCTCTATATCACTTAATCTCATCTTGTCTGGAACCCATTCTACAGAACACA 2283
 OY 2297 TTCCCAACAGTACCAAGCTGAAGGCTCTCATGACGAGGGACTTATTTGCAGTGC 2356
 DB 2284 TTCCCAAGTATACCAAGGCTGCGGCTCTCATGACGAGGGACTTATTTGGAATGC 2343
 OY 2357 CCAGAGAGAAAGCAACGCTGGCTCTTTGGGCTTAACATTAAGCCGCTTTTAATATGA 2416
 DB 2344 CTACTGAGAGGGAAGGCAAGCTGGCTTTTGGGCCAAGCTTAGAGCTTATTAATGA 2403
 OY 2417 AATTACACTTACTGCTGAAAACAATGATGTGAATCTTAAAAAATTTAGAAAAATTCA 2476
 DB 2404 AGTTAGCTTGTGTCATG---AGGATGATGTGAATAAATTGAAA---CTTGGGTTTCTGA 2456
 OY 2477 CTTAAGAAACCATTTTACTTGGATGATGATGATGATGATGATGATGATGATGATGATG 2536
 DB 2457 CTTAATTAAC---TGTCAACCTGGGCTCTCATGAACACGTGGTTTTCAGTTCTTACCC 2513
 OY 2537 GAGTGCTCTCATTAAT 2552
 DB 2514 GAGGTACTTCTGTCT 2529
 RESULT 13
 ADU23193
 ID ADU23193 standard; cDNA; 2421 BP.
 AC ADU23193;
 XX 27-JAN-2005 (first entry)
 DT
 XX Murine Toll-like receptor 6 (TLR6) cDNA sequence - SEQ ID 85.
 DE
 XX screening; Toll-like receptor agonist; TLR agonist; gene; ss; TLR6.
 KM
 XX Mus sp.
 OS
 PN MO2004094671-A2.
 XX
 PD 04-NOV-2004.
 XX
 PF 22-APR-2004; 2004WO-US012788.
 XX
 PR 22-APR-2003; 2003US-0464586P.
 PR 22-APR-2003; 2003US-0464586P.
 XX
 PA (COLE-) COLEY PHARM GROUP INC.
 PA (COLE-) COLEY PHARM GROUP INC.
 PI Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
 XX WPI: 2004-795573/78.
 XX
 PT Identifying agonists of Toll-like receptor (TLR) signaling activity,
 useful therapeutically or prophylactically, comprises contacting an

PT RPM18226 cell that expresses a TLR with a test compound and measuring TLR
 PT signaling activity.
 XX
 PS Disclosure; SEQ ID NO 85; 342bp; English.
 CC The invention comprises a screening method for identifying agonists of
 CC Toll-like receptor (TLR) signaling activity. The method involves
 CC contacting an RPM18226 cell (that expresses a TLR) with a test compound,
 CC and measuring a test level of TLR signaling activity, where a test level
 CC that is positive is indicative of a test compound that is a TLR agonist.
 CC The method of the invention is useful for identifying agonists of TLR.
 CC The present nucleic acid represents a TLR cDNA sequence.
 SQ Sequence 2421 BP; 640 A; 586 C; 521 G; 674 T; 0 U; 0 Other;
 Query Match 55.6%; Score 1531.2; DB 13; Length 2421;
 Best Local Similarity 77.6%; Pred. No. 0;
 Matches 1848; Conservative 0; Mismatches 533; Indels 0; Gaps 0;
 63 CATCATGACCAAGCAAGAACCTATTTGTTAAAGCTTTCATTTTGGCTTATGAT 122
 DB 30 CAACATGAGCCAGACAGAAACCCATGCTGGGAGTTTCCATTTGTTGGCCCTGAC 89
 OY 123 CATATATGTTGGAAACCAAGATCCAGTTCTCCGACGGAATGAAATTTGCAAGACATC 182
 DB 90 CTTATATGTCGGAACATGACCCCGTTCTTAATGAACCTGATGATGATGATGATGATG 149
 OY 183 AAAAAGAGCTTATTCATGTTCCAAAGAACCTACGCTGAAACCAAGCTTATGATAT 242
 DB 150 AAACAGGAACCTTATCTATGTCCTCCAAAGACCTGCACCAAGAACAAAGGCTGATCT 209
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 OY 303 AGTTTGAAGCTTTCCCAACAGATCCAGCTACTTATGATTTAAAGTTTTCAAGTCA 362
 DB 270 AGTTCTGAGACTCTCCCAACAGATGAGAGCTTATTTCCATGATTTCTTGTCA 329
 OY 363 CCAGATTTGAATATTTGATTTATCTCATATATCAGTTGCAAAAGATATCTGCAATCC 422
 DB 330 TCAGGACTTAAGATATCTGATGATCTCACACATGCTGGAACAAATCTCTTGTGCCC 389
 OY 423 TATTTGAGTTTCAGGCAATTTGATCTCTCATTTCAATGATTTCAAGGCCCTGCCATCTG 482
 DB 390 TATGCGAGCTGAGGCAATCTGACCTCTCATTAATCACTTGAATGATGCTGCTGTG 449
 OY 483 TAAAGATTTGGCAACTATATCAAACTGAATTTCTTGGATTTGAGTGTGCTATGAC 542
 DB 450 TAAAGATTTGGCAACTATATCAAACTGAATTTCTTGGATTTGAGTGTGCTATGAC 509
 OY 543 AAAATTAAGATTTGCTGCCAATTTGCTCACTTGCATCTTAAGTTATATCTTGTGATTTAAG 602
 DB 510 ACAACTGATCTGCTCCAGATTGCTCACTTGCATCTTAAGTTATATCTTGTGACTTATG 569
 OY 603 AAATTAATTAATTAAGAAATGAGACAGAAAGTCTAATAATTTCTGAATGCAAAACCT 662
 DB 570 GAGTTATCAATTAAGAAAGGCGGAGAAACGAAAGTCTCAATTTCCCAATACACCGTTCT 629
 OY 663 TCACCTGTTTTCACCCCACTAATTTATTTGCTATCCAAAGTGAACATATGATTAATAC 722
 DB 630 CCAATTTGCTCTTATCTCAATTAAGTCTTCTGCTTCAATGATGATGATGATGATGATG 689
 OY 723 TTAAGGCTGTTAAGTCACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 782
 DB 690 TTTAGGACATTTAAGTCACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 749
 OY 783 TAAATTTTATCAAGTCACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 842
 DB 750 GACATTTTATCAAGTCACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 809
 OY 843 AGAAAGCACTTGAAGTCCGTGACAGTCTTCAATTTCTTGGCCAAACCTGTGGA 902

Db 810 AGAAAACAACCTGGAAGTCTGGTTAACTTTTCCAAATCTTTTGSCCCCGACCGGTGGA 869
 Qy ATATCTCAATATTATTAACAATTTAAACAATATTGAAGACATGGTGAAGAAATTTTACTTA 962
 Db 870 GTACCTCAATATTATTAACAATTTAAACAATATTGAAGAAATCGACAGGAAATTTTACTTA 929
 Qy 963 TTTTAAACGACATTTGAAGACATTTGACATATGACATATCAAGAACCAAGTTTTCTGT 1022
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 Qy 1023 TTCACAGACGCTTTGTACCCGTTTCTTTCAGATGAAATTAATGATTTTAAACATTTTC 1082
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 Qy 1083 AGATACACCTTTTATACACATGCTGTCTCATGACACCAAGACATTTCAAGTTTTTGA 1142
 Db 1050 AGACACCCCTTTTATCACAATGTGTGCGCCATCCCAAGCTATTTTACATTTCTGA 1109
 Qy 1143 CTTTACCAGAAACGTTTTACAGATATGATTTTGAATAATGTTCCAGCTTAGTTAAAT 1202
 Db 1110 CTTTACCAGAAATGTTTTTATGACAGTGTTTTCAAGGCTGTTCCACTTAAAGAT 1169
 Qy 1203 GGAGACATTTTCTTACAAAAAATGATTTAAAGACCTTTTCAAAATGATCTATGAC 1262
 Db 1170 GCAGACCTTTATCTTACAAAGAAATGTTGAAGAACTTTTAAAGTAGCTCATGAC 1229
 Qy 1263 GAAGATATGCTCTTTGAAAAATATGAGATTTAGTGTGTTAAATTTGCTTCAAAAT 1322
 Db 1230 TAAAGATATGCTCTCTGAAACCTTTGATTTGATTTGATTTGATTTGATTTGATTTG 1289
 Qy 1323 ACATTAAGAAAACTGACATTTGGGTTGAAGATATGATTTGTTAAATTTGCTTCAAAAT 1382
 Db 1290 ATATGACAGGACATGCGCTGGGCTGAGAGCATATTTGGTGTGAATTTGCTTCAAAAT 1349
 Qy 1383 GCTTACTGACTGTGTTTCAAGTGTTTTACTCTCCAGATCAAGATGATTTTCAAG 1442
 Db 1350 GCTTACAGGCTGTGCTTCAAGTGTTTTACTCTCCAGATCAAGATGATTTTCAAG 1409
 Qy 1443 CAATTAATTAAGAGCGTTCCCTTAAACAAGTCTTAAACCTGAAGCTTTGCAAGAACTCA 1502
 Db 1410 CAACAGATTAATGACATCTCTTAAAGATGTCACCACTGACAGGCTTTGCAAGAACTCA 1469
 Qy 1503 TGTGCTTTCAATTTTAACTGACCTTCTGATGTGGCAGCTTTAGACGCTTTCTGT 1562
 Db 1470 TGTACATCAACATCTCTTAACTGACCTTCTGATGTGGGCTTCAAGAGCTTTCTGT 1529
 Qy 1563 ATTGATCATGATTCACATTCAGTTTCCCAACCAATGCTGATTTTCTTCAAGCTGCCA 1622
 Db 1530 GCTGCTCATCGACCAATCACTGATTTCCATCTCTGAGATTTTCTTCAAGAGCTGCA 1589
 Qy 1623 GAAGATGAGGTCAATTAAGAGAGGAGCAATTCATTTCCATGATGACCTGAGCTTAAGAGA 1682
 Db 1590 GAATTTGATGATCCCTTAAACGCGGAAACCAACCATTTCCATGACATGAGCTGAGGGA 1649
 Qy 1683 ATTGCTCAAAAAATATAGCAAGATCAAGTGAAGTGAAGGCGTGGCTGATTTCTTA 1742
 Db 1650 CTTTGTCAAGAAACATAGGCTGGGTAGCAAGAAAGTGGAGGCTGGCTGACCTCTTA 1709
 Qy 1743 TAACTGTGATCCCAAGAAATGATTAAGAGAAAGCCCACTTAAAGACTTTCAATGTCTCA 1802
 Db 1710 CAGGTGTGATCAACCGAAAGCTCTTAAGGGAATGCACTGAGGGAATTTCCACATATCTCC 1769
 Qy 1803 ATTATCTGCAACATTAATCTGCTGATGCTGACATCGGTGTCACATGCTGATGTGGC 1862
 Db 1770 ACTGTCTGTGATATCTGTTCTGCTGATCTGACATCGGAGGCACTATGCTGTGGC 1829
 Qy 1863 TGTGACTGTGACCTGCTCTGCTGATCTACTTGTGATCTGATGATGATGATGATGATG 1922
 Db 1830 TGTGACTGTGGGCTTCTCTGCTGATCTGATGATGATGATGATGATGATGATGATG 1889
 Qy 1923 CCAGTGAACCCGATCTGGCGGAGGCGGAGAACTATCCCTTTGAAGAACTCCAAAGAA 1982
 Db 1890 TCAGTGAACACAGCACAGGCGGAGGCGGAGCAATCCCTTTGAAGAACTCCAAAGAA 1949

Qy 1983 CCTCCAGTTTCATGCTTTTATTTATATATAGTAAACATGATTTCTGCTGGGTGAAGTGA 2042
 Db 1950 COTCAGTTTCATGCTTTTATTTGCTCATACAGAGACATGATTTCTGCTGGGTGAAGTGA 2009
 Qy 2043 ATTGATCTTACTATGAAAAAAGATATCAATTTGCTTCTCATGAGAGAACTTTGT 2102
 Db 2010 ATTACTTACCAACCTTGAAGAAATGATACATCGGGTTTGCTCCATGAGAGAACTTTGT 2069
 Qy 2103 CCTCGCAAGACATTTGGAAGAAATATCATCACTGACATTTGAGAAAGTTTCAAGTCCAT 2162
 Db 2070 CCTCGCAAGACATTTGGAAGAAATATCATCACTGACATTTGAGAAAGTTTCAAGTCCAT 2129
 Qy 2163 CTTGTTTTGTCTCCCACTTTGTCCAGAGTGTGTGCTTATCGAATCTTATTTTGC 2222
 Db 2130 CTTGTGTGCTCTCCCACTTATCCAGAGAGTGTGTGCTTATCGAATCTTATTTTGC 2189
 Qy 2223 CCATCAACATCTCTTCTCATGAAAGATCTAATTAATCTTATCTCTCATGAGAAACCAT 2282
 Db 2190 CCATCATATATCTCTTCTCATGAAAGATCTAATTAATCTTATCTCTCATGAGAAACCAT 2249
 Qy 2283 TCCACAGAACAGCATTTCCCAACAGTACACACAGCTGAAGGCTCATGACGACGAGAC 2342
 Db 2250 TCTACAGAACACATTTCCAGTATGATACACAGCTGCGGCTCTCATGACGACGAGAC 2309
 Qy 2343 TTATTTGCAGTGCCCCCAAGGAAAGAAAGCGTGGCTCTTTGGGCTTAACTTTAGAC 2402
 Db 2310 TTACTTGAATGGCTACTGAGAAAGGCAACGTTGGGCTTTTGGGCAACTTATGAGC 2369
 Qy 2403 CGCTTTTATATGAAATTTAACAATGATCTGATGAGAAACATG 2443
 Db 2370 TTTCAATTTATGAAATTTAGCTTATGCTAATGAGAGTATG 2410

RESULT 14
 ADCT8820 standard; DNA; 2381 BP.
 ID ADCT8820 standard; DNA; 2381 BP.
 AC ADCT8820;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human PRO protein coding sequence #25.
 XX
 KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
 XX
 OS Crohn's disease; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003034984-A2.
 XX
 PD 01-MAY-2003.
 XX
 PF 15-OCT-2002; 2002WO-US033070.
 XX
 PR 19-OCT-2001; 2001US-0340083P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Goddard A, Gurney AL;
 XX
 DR WPI, 2003-481990/45.
 DR P-PSDB; ADCT8821.
 PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
 PT medicament for diagnosing or treating cancer or inflammatory bowel
 PT disorder e.g., ulcerative colitis or Crohn's disease.
 XX
 PS Claim 1; SEQ ID NO 49; 327bp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of human PRO
 CC proteins. The DNA and protein sequences of the invention are useful for
 CC the diagnosis and treatment of cancer and inflammatory bowel disease

CC (e.g. ulcerative colitis or Crohn's disease). The present DNA sequence
CC encodes a human PRO protein of the invention.
XX

Sequence 2381 BP; 725 A; 493 C; 450 G; 713 T; 0 U; 0 Other:

Query Match 52.5%; Score 1445; DB 10; Length 2381;
Best Local Similarity 76.3%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 550; Indels 6; Gaps 1;

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QY 84 ACCTATTGTTAAAGCTTCCATTTTGTGGCTTATGATCATATATGTTGAACCGAAT 143
DB 11 ATCCAGACATGACATCTTCATTTTCCATTTATCTTCACTGTTAATCTTCAGATCGAAT 70
QY 144 CCAGTCTCCGACGGAATGAAATTTGACAGACAGTCAAAAGAGCTTATTCATG 203
DB 71 ACAATTTATCGAAGAAAGTGAATTTTATGTTAGTCAAAAGAGCTTCAATCCACG 130
QY 204 TCCAAAAGACCTACCGCTGAAAAACAAAGCTTATGATATGTCAGAACTACATCGCTGA 263
DB 131 TCTTAAAGACCTATCCAGAAAACAAATCTTAATATATGCAAAATTTATATATCTGA 190
QY 264 GCTTCAGGCTCTGACATAGCTTTCTATCAGAGTTGACAGTTTGAGACTTCCATA 323
DB 191 GCTTGGACTTCTGACATCTTATCACTGCAAAACGAGAGATTTGATTAATTTCTATA 250
QY 324 CAGATCCAGCTACTGATTTAAGTGTTCAGATTCAACGAGATTTTGAATATTGGA 383
DB 251 TGAATCCAGTATCTTGATATACGTTTTCATTAATTCACAGAAATTTGAAATCTTGA 310
QY 384 TTATCTCATATACAGTTSCAAAAGATATCTGCCATCTTATTTGAGTTTCAAGCAT 443
DB 311 TTGTGCCACACAAGTTGGTGAAGATTTCTTGCCACCTACCTGTAACCTCAAGCAT 370
QY 444 AGATCTCTATTCATGATTTTCAAGGCTCCGCCATCTGTAAAGAAATTTGGCACTTATC 503
DB 371 GAACCTGTCATTTAAAGCATTTGATGCCCTGCTATATGCAAAAGATTTGGCAATATGC 430
QY 504 ACAAGCAATTTCTTGGGATGTGAGTCTAAGAGCTGCAAAATTTAGATTTGCTGCAT 563
DB 431 TCAATCAAAATTTCTGGGGGTGAGACCAACACTTAAGAAAATCTAGTGTCTGCAT 490
QY 564 TGTCTCATCTGATCTAAGTTATATCTCTGATTTTAAAGAAATTTATATATAAGAAA 623
DB 491 TGTCTCATCTGATCTAAGTTATATCTCTGATTTTAAAGAAATTTATATATAAGAAA 550
QY 624 TGAGACAGAAAGCTTACAAATTTCTGAATSCAAAACCTTCACTTGTTTTCACCAA 683
DB 551 AGACCTGAGGGCTTCAAGACTTTAAACCTGAGAGCTGCAATGTGTCCCCCAAA 610
QY 684 TAGTTTATCGCTATCCAGAGTACATCACTTAATCTTTAGGCTGTACAACTGAC 743
DB 611 CAAAGAAATTCATTTATTTTATTTGATGTGTCAGTCAAGACTGTAGCAAAATCTGAAATATC 670
QY 744 TAAATATTAAT-----TGAATGATGACAACTGCAAGTTTTCATTAATTTTATCAGA 797
DB 671 TAAATATCAATTTGTGCTAGAGATTAACAAATGTTTCTTACTTCTTAAGATTTCTGGCAA 730
QY 798 ACTCACAGAGGTTCACTTACGAAATTTTACCCCTCAACCAATAGAAAGCACTTGA 857
DB 721 ACTTCAAACTAACTCAAGTTATCAAGTCTTACCTTAAACAATGAAACAACCTTGA 790
QY 858 ATGCTGCTCAGAGCTTTCATTTCTTTGGCCCAACCTGTGGAATATCTCAATTTTA 917
DB 791 TTTCTTCAATAGGATCTCTCAGCTGTTGGCAATACACTGTATGATTTTCTCAATTTTC 850
QY 918 CAATTTAACAATATTTGAAGCATTCGTGAGAGAAATTTACTTATTTTAAACGACAT 977
DB 851 AAACGTGAAGTACAGGGTCACTGGAATTCAGAGATTTTGAATTTTCTGGACATTCCT 910
QY 978 GAAACATTTGACAAATAGACATATACGAAACAAGTTTCTGTGTTTTCACAGACCTTT 1037
DB 911 GAAAGCTTGTCTATACACCAAGATGTGTGAGCATGTGTGCTTCCGCAAAAGTTATAT 970
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QY 1038 GTACACCGTGTGTTTCTGAGATGAACATTAAGTTAACATTTGATGATACCTTTAT 1097
DB 971 CTAATGAATCTTTTGCATATGACATCAAAATTTTCAAGTCTGTGTAACGATGGT 1030
QY 1098 ACACATGCTGTGTCTCTACGACCAAGCACTTCAAGTTTGTGAACCTTACCAGACGT 1157
DB 1031 CCACATGCTTGTCCCATCCAAATATAGCCCGTCTCGCATTTGGATTTTCCAAATATCT 1090
QY 1158 TTTCAAGATAGATTTTGTGAAGAAATGTTCCAGCTTATAGTTAAATTTGAGACCTTATCT 1217
DB 1091 CTTAACAGACAGGTTTGTGAAGAAATTTGTGGACCTTACTGATTTGGAACCTTATTTT 1150
QY 1218 ACAAAAAATGATTTTAAAGACCTTTTCAAGAGGCTTCAGAGCAAGATATGCTTC 1277
DB 1151 ACAATATGATCAATTTAAAGAACTTTCAAAATAGCTGAATGATACACAGTGAAGTC 1210
QY 1278 TTTGGAATATCTGATGTTAGCTGGAATTTCTTGAATCTGTGATGACATTAAGAAACCTG 1337
DB 1211 TCTGCAACAAATTTGATATTTAGCAGAAATTTCTGATGCTATGATGAAGAAAGAGACTG 1270
QY 1338 CACTGGCTTGAAGATATGCTGTAAATTTGCTTCAATATGCTTACTGACTCTGT 1397
DB 1271 TTTCTGACTTAAAGATTTATTAAGTTAAATATGCTTCAAAATATATCTTACTGACACTAT 1330
QY 1398 TTTCAAGATTTTACCTCCAGGATCAAGGATCACTTCAACAGCAATTAATAAGAG 1457
DB 1331 TTTCAAGATTTTACCTCCAGGATCAAGGATCACTTCAACAGCAATTAATAAGAG 1390
QY 1458 CTTTCTTAAACAAGTCTTAAACCTGGAACCTTTGCAAGAACTCAATGTTGCTTCAATTC 1517
DB 1391 CATTCTTAAACAAGTCTTAAACCTGGAACCTTTGCAAGAACTCAATGTTGCTTCAATTC 1450
QY 1518 TTTTAACTGACCTTCTGATGTGAGAGCTTTAGCAAGCTTTCTGATTTGATCATTTGATCA 1577
DB 1451 TTTTAACTGACCTTCTGATGTGAGAGCTTTAGCAAGCTTTCTGATTTGATCATTTGATCA 1510
QY 1578 CAATTCAGTTTCCACCCCATCGGCTGATTTCTTCCAGAGCTCCAGAAATAGGTCAT 1637
DB 1511 CAATTCAGTTTCCACCCCATCGGCTGATTTCTTCCAGAGCTCCAGAAATAGGTCAT 1570
QY 1638 AAAACAGGGGCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1697
DB 1571 AAAACAGGGGCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1630
QY 1698 AGACCAAGTATCAAGTGAAGTGTGAAGGGCTGCTGATTTCTTAAAGTGTGACTACCC 1757
DB 1631 AGACCAAGTATCAAGTGAAGTGTGAAGGGCTGCTGATTTCTTAAAGTGTGACTACCC 1690
QY 1758 AGAAGTTATAGAGAGCCCATTAAGGACCTTCAACATGCTGAATTAATCCTGCAACAT 1817
DB 1691 GGAAGTTATAGAGAACCTTCAAGGACCTTCAACATGCTGAATTAATCCTGCAACAT 1750
QY 1818 AACTGCTGATCGTCAACATCGGTGCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1877
DB 1751 AACTGCTGATCGTCAACATCGGTGCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1810
QY 1878 CCTGTCATCTACTTGGATCTGCTGCTGATCTCAAGATGTGTGCCAGTGAACCCAGAC 1937
DB 1811 CCTGTCATCTACTTGGATCTGCTGCTGATCTCAAGATGTGTGCCAGTGAACCCAGAC 1870
QY 1938 TCGGGCGAGGGCAGAGAACATTCCTTGAAGAACTTCCAAAGAAACCTCCAGTTTCAATG 1997
DB 1871 CCGGGCGAGGGCAGAGAACATTCCTTGAAGAACTTCCAAAGAAACCTCCAGTTTCAATG 1930
QY 1998 TTTTATTTCAATATGTAACATGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2057
DB 1931 ATTATTTCAATATGTAACATGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1990
QY 2058 AGAAAAAGAGATATACAGATTTGCTTCAAGAGAACTTTTGTCCCTGCGCAAGACAT 2117
DB 1991 AGAGAAAGAGATATACAGATTTGCTTCAAGAGAACTTTTGTCCCTGCGCAAGACAT 2050
QY 2118 TGTGAAAAATATCATCACTGATGAGAGAGTTTAAAGTTCATCTTGTGTTGTCTCC 2177
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Db      2051 TGTGAAAAATATCATTCACCTGATGAGAGAGTTACAGTCATCTTTGTTTGTCTCC 2110
Qy      2178 CAACCTTTTCCAGAGTGTGTGCTGCTTACGAACCTATTTTGGCCATTCACATCTCTT 2237
Db      2111 CAACCTTTTGTCCAGAGTGTGTGCTGCTTACGAACCTATTTTGGCCATTCACATCTCTT 2170
Qy      2238 TCATGAGAGATCTATTAATCTTAATCTTCATCTTACGAAAGCCATTCCAGAAAGAGAT 2297
Db      2171 TCATGAGAGATCTATTAATCTTAATCTTCATCTTACGAAAGCCATTCCAGAGTACTCAT 2230
Qy      2298 TCCCAACAGATACCAAGAGTGAAGGCTCTCATGACGAGCGGACTTATTGCACTGCGC 2357
Db      2231 TCTTAGCGATTATACAGAGCTCAAAAGTCTCATGCGCAGAGAGACTTATTGGAATGCGC 2290
Qy      2358 CAAGAGAAAGAAAGCAAGCTGGGCTCTTTTGGGCTAACTTGAAGCGGCTTTAATATGA 2417
Db      2291 CAAGAGAAAGAGCAAGCTGGGCTTTTGGGCTAATTAAGGAGGCAATTAATATTA 2350
Qy      2418 ATTACA 2424
Db      2351 GCTGACA 2357

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RESULT 15

ADE25536
ID ADE25536 standard; DNA; 2358 BP.

AC ADE25536;

XX 29-JAN-2004 (first entry)

XX Human TLR1 related DNA SEQ ID NO 2.

XX Human, TLR1; cancer; cytosstatic; ds; gene.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..2358

FT FT /tag= a

FT FT /product= "TLR1"

FT FT /partial

FT FT /note= "the CDS lacks a stop codon"

XX MO2003061697-A1.

XX 31-JUL-2003.

XX 26-DEC-2002; 2002WO-JP013642.

XX 27-DEC-2001; 2001JP-00398165.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Hikichi Y, Katsuyama R, Kakoi Y, Nishizawa S;

XX WPI: 2003-598709/56.

XX P-PSDB; ADE25535.

XX Treatment and prevention for cancer of the e.g. digestive system, liver

XX and lung.

XX Disclosure; Page 80-84; 98pp; Japanese.

XX The invention relates to the treatment and prevention of cancer

XX comprising a compound that inhibits the activity of protein or peptide

XX fragment of a fully defined amino acid sequence TLR1 given as SEQ ID NO

XX 1. TLR1 is useful in the treatment and prevention of cancers of the large

XX intestine, mammary glands, lung, prostate, digestive tract, stomach and

XX liver. TLR1 gene expression is detected in breast cancer tissue. The

XX present sequence is that of a human TLR1 encoding DNA sequence.

Seq Sequence 2358 BP; 720 A; 486 C; 444 G; 708 T; 0 U; 0 Other;

Query Match 52.5%; Score 1444.2; DB 10; Length 2358;

Best Local Similarity 76.4%; Pred. No. 0;

Matches 1789; Conservative 0; Mismatches 548; Indels 6; Gaps 1;

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Qy      88 ATTGTTAAAGCTTCCATTTTGTGCTTATGATCATATATGTTGGAACCAATATCAG 147
Db      1 ATGACTAGCATCTTCATTTTGGCCATTATCTTCATGTTAAATCTTCAGATCAGATACAA 60
Qy      148 TTCTCCACGGAATGGAATTTGCAAGTGAACAAGCAAAAGAGGCTTATTCATGTTCCA 207
Db      61 TTATCTGAAGAAAGTGAATTTTAAAGTATGATGATGATGATGATGATGATGATGATGAT 120
Qy      208 AAAGACCTACCGCTGAAGAAACCAAGCTTATGATATGTTCTAGAACTACATGCTGAGCTT 267
Db      121 AAAGACCTATCCGAGAAACCAAGCTTATGATATGATGATGATGATGATGATGATGATGAT 180
Qy      268 CAGGCTCTGACATGAGCTTCTATCAGAGTTGACAGTTTGAACCTTCCATTAACGA 327
Db      181 TGGACTTCTGACATCTTATCAGTGTCAAAAGTGAAGATTTGATTAATTTCTCATTAATGA 240
Qy      328 ATCCAGCTACTGATTAAGGTTTTCAGTTCAACGAGATTTAGAAATATTTGGAATTA 387
Db      241 ATCCAGTATCTTGATATCAGTGTTCAGTTCAACGAGATTTGGAATATTTGGAATTTG 300
Qy      388 TCTCATATCAGTTGCAAAAGATATCCGCTCATATTTGATGATTTGAGGCACTTATGAT 447
Db      301 TCCCAACCAAGTTGATGATATTTCTTCCACCTCATGATGAACTTCAACGACTTGGAC 360
Qy      448 CTTCATTCATTAATGATTAAGGCTTCCATCTGATTAAGGATTTGGCACTTATACAA 507
Db      361 CTGTCATTTTAATGATTTGATGAGCTTGTATGATGATGATGATGATGATGATGATGATGAT 420
Qy      508 CTGGAATTTCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567
Db      421 CTGGAATTTCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Qy      568 CACTTCATCTAATGATTAATCTTGTGATTTAAGAAATTTATATTAATTAAGAAATGAG 627
Db      481 CATTTGAATATCAGCAAGCTCTTGTGATTTAAGAAATTTATATTAATTAAGAAATGAG 540
Qy      628 ACAGAAAGCTAACAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687
Db      541 CCGAGGAGCTTCAAGATTTAACAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 600
Qy      688 TTATTCGCTATCAAGTGAACATATCAAGTGAACATATCAAGTGAACATATCAAGTGAAC 747
Db      601 GAATTCATTTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Qy      748 ATTAAAT-----TGATGATGACAACTGCAAGTTTCAATTAATTTTATCAAGATCTC 801
Db      661 ATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Qy      802 ACCAGAGTTCAACCTTAAGTGAATTTTACCTCAACCAAGTGAACATTTGGAATATG 861
Db      721 CAACAAATCCAAAGTATCAAGCTTCACTTAAACCAATGGAACCACTGGAATCT 780
Qy      862 CTGCTCAAGCTTCTTCAATTTCTTGGCCAAACCTGGAATATCTCAATATTAACAT 921
Db      781 TTCAATTAAGATCTTCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Qy      922 TTAACAATATTAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 981
Db      841 GTGAAGCTACAGGCTCAGCTGATCTCAAGATTTTGAATTTTCTGGAATCTCTTGAAG 900
Qy      982 GCATTGACATTAAGCAATATCAAGCAAGATTTTCTGTTTCAACAGACCTTTGAC 1041
Db      901 GCTTGTCTAATACCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Qy      1042 ACCGCTTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1101
Db      961 GAATCTTTTGAATATGAACATCAAAATTTCAAGTGTCTGATGATGATGATGATGATGATGAT 1020

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QY 1102 ATGCTGTGCTCATGACCAACACATTCAGTTTGTGAACCTTACCCAGAACGTTTTC 1161
 DB 1021 ATGCTTGGCCATCCAAATATAGCCGTTCTGCAATTTGGATTTTCCAAATATCTCTTA 1080
 QY 1162 ACAGATAGTATTTTGAATAATGTTCCACGTTAGTTAAATGGAGACACTTATCTTACA 1221
 DB 1081 ACAGACACGCTTTTGAATAATGTTGGCACCTTACTGAGTTGGAGACATTAATTTACAA 1140
 QY 1222 AAAAATGATTAAGAAACCTTTTCAAGAGTCTATGACGAGAGATATGCTTTTGG 1281
 DB 1141 AAGAATTCATTAAGAAACCTTTTCAAGAAATGAGTGAATGACAGATGAAGTCTCTG 1200
 QY 1282 GAATATCTGATGTTGATGTAATCTTGTGAATCTGTAGACATTAAGAAAACCTGACT 1341
 DB 1201 CAACAATTTGATTAATGACGAATTTCTGAAGCTATGATGAAGAAAGAAAGAGCTGTTCT 1260
 QY 1342 TGGGTGAGAGTATAGTGTGTTAAATTTGTCTTCAATATGCTTACTGACTCTGTTTC 1401
 DB 1261 TGGACTAAAGTTTATTAAGTTTAAATATGTTCTTCAATATATCTGACACTATTTTC 1320
 QY 1402 AGATGTTTACCTCCAGAGTCAAGGTACTTGTATCTTCAAGCAATTAATTAAGACGTT 1461
 DB 1321 AGATGTTTACCTCCAGAGTCAAGGTACTTGTATCTTCAAGCAATTAATTAAGACGATT 1380
 QY 1462 CCTAAACAAGTGTAAACCTGAAGCTTGGCAAGAACTCAATGTTGCTTCAATCTTAA 1521
 DB 1381 CTTAAACAAGTGTAAACCTGAAGCTTGGCAAGAACTCAATGTTGCTTCAATCTTAA 1440
 QY 1522 ACTGACCTTCTGATGTTGGCAGCTTTTACAGCCCTTCTGTATTTGATCATTTGACAAAT 1581
 DB 1441 ACTGACCTTCTGATGTTGGCAGCTTTTACAGCCCTTCTGTATTTGATCATTTGACAAAT 1500
 QY 1582 TCAAGTTTCCACCCATCGGCTGATTTCTTCCAGAGCTGCCAGAAAGTAGGTCAATAAA 1641
 DB 1501 TCAAGTTTCCACCCATCGGCTGATTTCTTCCAGAGCTGCCAGAAAGTAGGTCAATAAA 1560
 QY 1642 GCAGGGGACAATCCATTCCAATGTAACCTGTGAGCTAAGAGAAATTTGTCAAAAATATAGAC 1701
 DB 1561 GCAGGGGACAATCCATTCCAATGTAACCTGTGAGCTAAGAGAAATTTGTCAAAAATATAGAC 1620
 QY 1702 CAAGTATCAAGTGAAGTGTTAAGAGGCTGGCCTGATTTCTTATAGTGTGACTACCCAGAA 1761
 DB 1621 CAAGTATCAAGTGAAGTGTTAAGAGGCTGGCCTGATTTCTTATAGTGTGACTACCCAGAA 1680
 QY 1762 AGTTATAGAGAAAGCCCACTAAAGACTTTCACATGCTGAATTAATCTGCAACATACT 1821
 DB 1681 AGTTATAGAGAAAGCCCACTAAAGACTTTCACATGCTGAATTAATCTGCAACATACT 1740
 QY 1822 CTGCTGATGCTGACCATGCGTGGCCCAAGCTGTGTTGGCTGTGACTGTGACCTCCCTC 1881
 DB 1741 CTGCTGATGCTGACCATGCGTGGCCCAAGCTGTGTTGGCTGTGACTGTGACCTCCCTC 1800
 QY 1882 TGCATCTACTTGGATCTGCTCCGTGATCTCAGGATGCTGTGCAAGTGAACCCAGACTCG 1941
 DB 1801 TGCATCTACTTGGATCTGCTCCGTGATCTCAGGATGCTGTGCAAGTGAACCCAGACTCG 1860
 QY 1942 CGCAGGGCCAGGAACATACCTTTAGAAGAACTTCAAGAAACCTCCAGTTTCATGCTTTT 2001
 DB 1861 CGCAGGGCCAGGAACATACCTTTAGAAGAACTTCAAGAAACCTCCAGTTTCATGCTTTT 1920
 QY 2002 ATTTTCATATAGTGAACATGATCTGCTGCGGTGAAGAAAGTGAATGGTACTTACTTAGAA 2061
 DB 1921 ATTTTCATATAGTGAACATGATCTTTCGCGGTGAAGAAAGTGAATGGTACTTACTTAGAA 1980
 QY 2062 AAAGAAGATATACAGATTTGCTTTCATGAGAGAACTTTGCTCCGCAAGAGCATTTGTG 2121
 DB 1981 AAAGAAGATATACAGATTTGCTTTCATGAGAGAACTTTGCTCCGCAAGAGCATTTGTG 2040
 QY 2122 GAAATATATCATCACTGCAATTAAGAGAGTTACAAGTCACTTTGTTGTTGCTCCCAAC 2181
 DB 2041 GAAATATATCATCACTGCAATTAAGAGAGTTACAAGTCACTTTGTTGTTGCTCCCAAC 2100

QY 2182 TTGTCCAGAGTAGAGNGTGCCATTACGAACCTTAATTTTGGCCATCAACATCTTTTCAAT 2241
 DB 2101 TTGTCCAGAGTAGAGNGTGCCATTACGAACCTTAATTTTGGCCATCAACATCTTTTCAAT 2160
 QY 2242 GAAGATCTAATTAATTAATCTTCAATCTTACTGGAACCCATTCCACAGAACGATTTCC 2301
 DB 2161 GAAGATCTAATTAATTAATCTTCAATCTTACTGGAACCCATTCCAGAACGATTTCC 2220
 QY 2302 AACCAATCAACAACTGAAGCTCTCATGACGCGAGCGGACTTAATTTGAGTGGCCCAAG 2361
 DB 2221 ACCAGTTTCAACAACTGAAGCTCTCATGACGCGAGCGGACTTAATTTGAGTGGCCCAAG 2280
 QY 2362 GAGAAAGCAACGTTGGCTTTTGGGCTAATTAAGAGCCGCTTTTAATTAAGAAATTA 2421
 DB 2281 GAAAGAGCAACGTTGGCTTTTGGGCTAATTAAGAGCCGCTTTTAATTAAGAAATTA 2340
 QY 2422 ACA 2424
 DB 2341 ACA 2343

Search completed: June 4, 2006, 23:39:59
 Job time : 1689 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2006, 23:18:43 ; Search time 15573 Seconds
(without alignments)
11304.646 Million cell updates/sec

Title: US-10-732-796A-11
Perfect score: 2753
Sequence: 1 agaatcgcacatcatca.....ttcccaatgcattctgtg 2753

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 636136 seqs, 31973710525 residues
Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb env: *
2: gb pat: *
3: gb ph: *
4: gb pl: *
5: gb pr: *
6: gb ro: *
7: gb sts: *
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9: gb un: *
10: gb vi: *
11: gb ov: *
12: gb htg: *
13: gb in: *
14: gb om: *
15: gb ba: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2749.8	99.9	2758	2	CQ726557
3	2749.8	99.9	2758	2	AR659471
4	2749.8	99.9	6758	2	AR659631
5	2749.8	99.9	6758	2	AR659757
6	2749.8	99.9	173834	5	AC108044
7	2748.8	99.8	2760	2	CQ870747
8	2748.8	99.8	2760	2	CQ903892
9	2748.8	99.8	2760	2	AR659345
10	2748.8	99.8	2760	2	AX399047
11	2748.8	99.8	2760	2	AB020807
12	2748.2	99.8	78986	12	AC115626
13	2748.2	99.8	183019	12	AC115626
14	2747.2	99.8	2760	2	E34464
15	2727.8	99.1	2940	2	AX576262
16	1925.2	69.9	173804	14	AB210286
17	1907.2	69.3	194826	12	AC163791
18	1860.2	67.6	2559	14	AB208698

19	1787.8	64.9	2919	14	AJ620670
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21	1783	64.8	2391	14	AB085936
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24	1540.4	56.0	193583	6	AC161757
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ALIGNMENTS

RESULT 1
LOCUS CQ903893 2753 bp DNA linear PAT 16-NOV-2004
DEFINITION Sequence 79 from Patent WO2004094671.
ACCESSION CQ903893
VERSION CQ903893.1 GI:55785292
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 Vollmer, J., Jurk, M., Lipford, G.B., Schetter, C., Forsbach, A. and
Krieg, A.M.
TITLE Methods and products for identification and assessment of tlr
ligands
JOURNAL Patent, WO 2004094671-A 79 04-NOV-2004;
Coley Pharmaceutical GmbH (DE); Coley Pharmaceutical Group, Inc.
(US)

FEATURES
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	AAACATGACCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120
DB	61	AAACATGACCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120
QY	121	ATCAATATAGTTGGAAACGAGATCCAGTCTCCGACGGAATGATTTGACATGACAAAG	180
DB	121	ATCAATATAGTTGGAAACGAGATCCAGTCTCCGACGGAATGATTTGACATGACAAAG	180

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DEFINITION CQ726557.1 GI:42289938
VERSION CQ726557.1 GI:42289938
KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
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thereof

JOURNAL Patent: WO 02068579-A 12491 06-SBP-2002;

FEATURES
PE Corporation (NY) (US)

LOCATION/Qualifiers
1..2758

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RESULT 4

AR659631 6758 bp DNA linear PAT 13-JUN-2005
LOCUS AR659631 Sequence 672 from patent US 6900016.
ACCESSION AR659631
VERSION AR659631.1 GI:67595671
KEYWORDS
SOURCE
ORGANISM

REFERENCE

1 (bases 1 to 6758)
Unclassified.
Venter, J.C., Zhang, J.N., Liu, X., Rowe, W., Cravchik, A., Kalush, F.,
Nalk, A., Subramanian, G. and Woodage, T.
Polymorphisms in known genes associated with inflammatory
autoimmune disease, methods of detection and uses thereof
Patent: US 6900016-A 672 31-MAY-2005;
Aplera Corporation; Norwalk, CT

FEATURES

source
1..6758
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 99.9%; Score 2749.8; DB 2; Length 6758;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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LOCUS AF659757 6758 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 798 from patent US 6900016.
ACCESSION AR659757
VERSION AR659757.1 GI:67595817
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6758)
AUTHORS Venter, J.C., Zhang, J.N., Liu, X., Rowe, W., Cravchik, A., Kalush, F., Naik, A., Subramanian, G. and Woodage, T.
TITLE Polymorphisms in known genes associated with inflammatory autoimmune disease, methods of detection and uses thereof
JOURNAL Patent: US 6900016-A 798 31-MAY-2005; Aptera Corporation; Norwalk, CT
FEATURES
source location/Qualifiers
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ORIGIN
Query Match 99.9%; Score 2749.8; DB 2; Length 6758;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 6
AC108044/c 173834 bp DNA linear PRI 29-MAY-2002
DEFINITION Homo sapiens BAC clone RP11-280E3 from 4, complete sequence.
AC108044
AC108044.5 GI:20304050
KEYWORDS HTG.
SOURCE
Homo sapiens (human)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eularchontia; Eularchontia; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 173834)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
9847074
PUBMED
2 (bases 1 to 173834)
Nguyen, C., Abdolt, A., Bielicki, L. and Spalding, L.
The sequence of Homo sapiens BAC clone RP11-280E3
Unpublished (2001)
3 (bases 1 to 173834)
Waterston, R.H.
Direct Submission
Submitted (24-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 173834)
Waterston, R.H.
Direct Submission
Submitted (25-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 173834)
Waterston, R.H.
Direct Submission
Submitted (29-MAY-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Apr 25, 2002 this sequence version replaced gi:20128729.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH02800303

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
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Best Local Similarity 99.9%; Pred. No. 0;
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QY 121 ATCTAATATGTTGGAACCAAGATCCAGTCTCCGACCGAAATGAATTTGACGTAGACAG 180
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ACCESSION      CO870747
VERSION      CO870747.1  GI:52000200
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SOURCE      unidentified
ORGANISM      unidentified
REFERENCE      1. unclassified sequences.
AUTHORS      Hardiman, G.T., Rock, F.L., Bazan, J.F., Kastelein, R.A., Ho, S.W. and
              Liu, Y.J.
TITLE      Human receptor proteins, related reagents and methods
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LOCUS AR659345
DEFINITION Sequence 100 from patent US 690016.
ACCESSION AR659345
VERSION AR659345.1 GI:67595337
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2760)
AUTHORS Venter,J.C., Zhang,J.N., Liu,X., Rowe,W., Cravchik,A., Kalush,F.,
Naik,A., Subramanian,G. and Woodage,T.
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autoimmune disease, methods of detection and uses thereof
JOURNAL Patent: US 690016-A 100 31-MAY-2005;
Applera Corporation; Norwalk, CT
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Matches 2750; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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VERSION AX399047.1 GI:21261430
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE
 1 (sites)
 Takeuchi, O., Kawai, T., Sanjo, H., Copeland, N.G., Gilbert, D.J.,
 Jenkins, N.A., Takeda, K. and Akira, S.
 TLR6: A novel member of an expanding toll-like receptor family

JOURNAL
PUBMED
REFERENCE
AUTHORS

Gene 231 (1-2), 59-65 (1999)
10231569
2 (bases 1 to 2760)
Akira, S. and Takeuchi, O.

ORIGIN				
Query Match	99.8%	Score 2748.8;	DB 5;	Length 2760;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 2750; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0

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VERSION
HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
Homosapiens (human)
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
REFERENCE
1 (bases 1 to 78986)
AUTHORS
Waterson,R.H.
TITLE
The sequence of Homo sapiens clone
JOURNAL
Unpublished
AUTHORS
2 (bases 1 to 78986)
TITLE
Waterson,R.H.
JOURNAL
Direct Submission
SUBMITTED (21-MAR-2002) Genome Sequencing Center, Washington
UNIVERSITY School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Mar 21, 2002 this sequence version replaced gi:8076856.

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: H_NH0685M06
Drafting center: WIBR
----- Summary Statistics -----
Sequencing vector: M13, 0%
Sequencing vector: plasmid, 100%
Chemistry: Dye-primer ET; 0% of reads
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Assembly program: Phrap; version 0.990319
Consensus quality: 64210 bases at least Q40
Consensus quality: 67703 bases at least Q30
Consensus quality: 69979 bases at least Q20
Insert size: 17700; agarose-fp
Insert size: 73365; sum-of-ctnigs
Quality coverage: 0.81 in Q20 bases; agarose-fp
Quality coverage: 2.05 in Q20 bases; sum-of-ctnigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 43 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1133 2884: contig of 1752 bp in length
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Homnidae; Homo.
1 (bases 1 to 182019)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 4, clone RP11-11518
Unpublished
2 (bases 1 to 182019)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavsky,L.,
Bouckagalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Chospel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
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TITLE
JOURNAL
REFERENCE
AUTHORS
Zody,M.
Direct Submission
Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 182019)
REFERENCE
AUTHORS
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Bouckagalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Chospel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
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Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
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Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Margulis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
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O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisan,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tefaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 12, 2000 this sequence version replaced gi:7229904.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 115.L.8
----- Summary Statistics
Sequencing vector: M13; W77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 158219 bases at least Q40
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Insert size: 133000; agarose-5p
Insert size: 179319; sum-of-contrigs
Quality coverage: 5.2 in Q20 bases; agarose-5p
Quality coverage: 3.8 in Q20 bases; sum-of-contrigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 28 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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LOCUS E34464 2760 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel Toll-like receptor and gene thereof.
ACCESSION E34464
VERSION E34464.1 GI:18624350
KEYWORDS JP 2000128900-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 2760)
 AUTHORS Shindra,S. and Takeuchi,S.
 TITLE Novel Toll-like receptor and gene thereof
 JOURNAL Patent: JP 2000128900-A 1 09-MAY-2000;
 SCIENCE & TECH AGENCY
 COMMENT OS Homo sapiens (human)
 PN JP 2000128900 -A/1
 PD 09-MAY-2000
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FEATURES
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ORIGIN

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 Matches 2749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DEFINITION Sequence 43 from Patent WO0162922.

ACCESSION AX576262
VERSION AX576262.1 GI:27646013
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Banville, S.C., Greenwalt, L.B., Lincoln, S.E., Stockbreher, T.K., Amshay, S., Chang, S.C., Chen, W., Dam, T.C., Liu, T.F., Rosen, B.H., Russo, F.D., D'Sa, S.A., Spiro, P.A., Bradley, D.L., Chen, A., Cohen, H.D., D'Alto, A., Daniels, S.E., Dutoit, G.E., Flores, V., Fong, W.T., Hodgson, D.M., Jackson, S., Jones, A.L., Panzer, S.R., Roseberry, A.M., Shah, P., Wright, R.J., Yap, P.E., Yu, J.Y., Bratcher, S.R., Chalup, M.S., Dahl, C.R., and Hillman, J.L.
TITLE Polypeptides and corresponding molecules for disease detection and treatment
JOURNAL Patent: WO 0162922-A 43 30-AUG-2001;
Incyte Genomics, Inc. (US)
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2006, 23:19:02 ; Search time 11668 Seconds
(without alignments)
13193.857 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est3:
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8: gb_est9:
9: gb_est10:
10: gb_est11:
11: gb_est12:
12: gb_est13:
13: gb_est14:
14: gb_est15:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1537.4	55.8	2550	6	AK137502 Mus muscu
4	1525.8	55.4	2388	14	AY416999 Mus muscu
5	1525.4	55.4	2522	6	AK154253 Mus muscu
6	1439.4	52.3	2806	6	HSN800268 AL050282 Homo sapi
7	1267.4	46.0	3051	10	DY109015 DY109015 001212BPM
8	1119.4	40.7	3020	6	AK143721 Mus muscu
9	604.8	22.0	1342	10	DV779572 Hw_Fac_64
10	571.4	20.8	573	9	DA673961 DA673961
11	562.4	20.4	564	9	DB143901 DB143901
12	553	20.1	609	9	DA619469 DA619469
13	529.8	19.2	772	2	BG963497 BG963497
14	527.2	19.2	698	8	CK980631 4112385 B
15	526.6	19.1	684	4	CB554647 CB554647
16	526	19.1	570	4	DA383103 DA383103
17	522.2	19.0	698	5	CK966621 CK966621
18	516	18.7	572	9	DA677587 DA677587
19	505.4	18.4	588	5	CD702179 EST18703

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21	480.2	17.4	525	2	BF925285	BF925285 RC3-NT015
22	476	17.3	677	12	CE100991	CE100991 tigr-gss-
23	472	17.1	695	4	BY763747	BY763747 BY763747
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25	462.6	16.8	630	12	CL003155	CL003155 gbs1_VMS_
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28	434.6	15.8	779	1	AM004250	AM004250 AM004250
29	429.2	15.6	485	7	BE006232	BE006232 RC2-BN012
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32	412.2	15.0	554	7	BF080760	BF080760 231760 MA
33	411.6	15.0	742	5	CD368967	CD368967 UI-H-FTL-
34	411	14.9	656	5	CF763276	CF763276 CES006083
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ALIGNMENTS

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VERSION
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TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
gene
ORIGIN

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AY416997
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GSS.
Homo sapiens (human)
Homo sapiens
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1 (bases 1 to 2391)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
Science 302 (5652), 1960-1963 (2003)
2 (bases 1 to 2391)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.
Direct Substitution
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment
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Query Match 86.7%; Score 2387.8; DB 14; Length 2391;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2389; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 ATGACCAAGACAAAGAACTTGTGTAAAGCTTCCATTTTGTGCTTATGATCA 60
QY 127 ATAGTTGGAAACAGATCCAGTTCTCCGACGAAATGAAATTCAGTAGACAGTCAAA 186
DB 61 ATAGTTGGAAACAGATCCAGTTCTCCGACGAAATGAAATTCAGTAGACAGTCAAA 120
QY 187 AGAGGCTTTATTCATGTTCCAAAAGACTTACCGCTGAAAACCAAGTCTTAATATGCT 246
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ACCESSION AY416998
VERSION AY416998.1 GI:39772958
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.

REFERENCE
AUTHORS 1 (bases 1 to 2391)
Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.D.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302

REFERENCE
AUTHORS 2 (bases 1 to 2391)
Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.D.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
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Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bull, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batilov, S., Beisel, K.W., Blake, J.A., Brad, D., Brusic, V., Chochla, C., Cordani, L.E., Cousins, S., Dalla, E., Dragan, T.A., Fletcher, C.F., Forrest, A., Fraser, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, J.J., Jarvis, E.D., Kanai, A., Kurochik, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempke, C.A., Setou, M., Shimada, K., Sulana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, K., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420 (6915), 563-573 (2002)

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Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Fritth, M.C., Mameda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Bremner, S.E., Batilov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Altans, V., Allen, J.E., Ambesi-Imponente, A., Apweiler, R., Atturay, R.N., Bailey, T.L., Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., Di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furum, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jaki, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochik, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan, B., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okasaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavese, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schombach, C., Sekiguchi, K., Sempke, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclaire, B., Spelling, S., Scuppa, E., Sugura, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamashita, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hilde, M., Bull, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori, K., Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Kono, H., Nakano, K., Nimomiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Wachihi, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.

PANTOM Consortium

The transcriptional landscape of the mammalian genome
Science 309 (5740), 1559-1563 (2005)

16141072

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AUTHORS
Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakashima, M., Nakamura, M., Nishida, H., Yagi, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Fritth, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batilov, S., Engstrom, P.G., Mizuno, Y., Feghli, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.

CONSRM
Riken Genome Exploration Research Group

TITLE
Antisense transcription in the mammalian transcriptome

JOURNAL
Science 309 (5740), 1564-1566 (2005)

PUBMED
16141073

AUTHORS
(bases 1 to 2550)
Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Kono, H., Murata, M., Nakamura, M., Nimomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Wachihi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
Direct Submissions

JOURNAL
Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsr.riken.jp).
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
location/Qualifiers

FEATURES
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Matches 1877; Conservative 0; Mismatches 566; Indels 0; Gaps 0;

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receptor 6, full insert sequence.
ACCESSION
AK154253
VERSION
AK154253.1 GI:74178406
KEYWORDS
HTC; CAP trapper.
SOURCE
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Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K.,
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Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, O., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, M., Gaasterland, T., Gissi, C., King, B., Kochwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Tomita, M.,
Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Holtman, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombauts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
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Tayo-oka, K., Wang, K. H., Weitz, C., Whitteker, C., Wilming, L.,
Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kotsuki, S.
and Hayashizaki, Y.
RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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Nikaido, I., Oseto, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schombach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Brdtk, D., Brasic, V.,
Chochia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,

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CONSRMT
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

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Nature 420 (6915), 563-573 (2002)

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COMMENT

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Riken Genome Exploration Research Group
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Science 309 (5740), 1564-1566 (2005)

8 (bases 1 to 2522)
16141073

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AUTHORS
Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Kono, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanabe, A., Muramatsu, M., and Hayashizaki, Y.

TITLE
JOURNAL
Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsukuba, Ibaraki, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome-gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL: http://genome-gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

FEATURES

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coll-like receptor 6 (MGI:1341296 GB) BC055366,
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ORIGIN

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DEFINITION   DY109015
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VERSION      DY109015.1 GI:86272292
KEYWORDS     EST.
SOURCE       Bos taurus (cattle)
ORGANISM     Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE    1 (bases 1 to 3051)
AUTHORS      McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
              Glenn,M., Hayukela,I., Watson,J., Crawford,A., Wheeler,T.,
              Hagemann,L., Lee,R., Hein,W., Johnstone,P., Magpool,N., McMahon,C.,
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              Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and
              Atkinson,P.
              AgResearch, Genesys and Primary Industry Victoria Bovine EST
              project
              Unpublished (2006)
              Contact: Magpool N
              AgResearch Ltd.
              Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
              Mosgiel, New Zealand
              Email: nauman.magpool@agresearch.co.nz.
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ORIGIN
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Matches 1644; Conservative 0; Mismatches 601; Indels 6; Gaps 1;

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QY 598 TTAGAAATTTATATATAAAGAAATGAGACAGAAAGTCTACAAATTTCTGAATGCAAA 657
DB 725 TTAGAGATATCTTATGGGAAAGAAAGATGCCGAGAGCTTCAACACTTAAAGACAG 784
QY 658 ACCCTTCACTTGTGTTTTCACCCCACTAGTTATTCGCTATCCAAAGTAAATATGAT 717
DB 785 AGCTGCACTTGTGTTTCCCAACAGAAAGAAATTCATTTATTTTGAACGTGTCAGTC 844
QY 718 AATCTTTAGGGTCTTACACTGATATATTTAAT-----TGAATGATGACACTGT 771
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QY 772 CAAGTTTTCATTAATTTTATCAGAACTCACAGAGTTTCAACTTGAATTTTACC 831
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DB 1145 GTGTTCAGTCTTCCAAAGTTATGTCTAATAAATTTGTCAAAATGTAACATCCAGCAT 1204
QY 1072 TTAAACATTTGAGATACACTTTTATACAGTGTGTCTCTACAGCAACAGACATTC 1131
DB 1205 CTCACAGTGTCTGTCGACACATGTCACATGCTGCCCCATCCCAATTTAGCCCATTT 1264
QY 1132 AAGTTTGAACCTTACCAGAAAGCTTTACAGATAGTATTTTGAATAATGTTCCAGS 1191
DB 1265 CTGTATTTGAATTTTTCATTAATCTTTTACAGACAGATTTTCTAATACTGTACAAAT 1324
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QY 1612 CAGAGTGCAGAAAGATGAGTCAATTAAGAGAGGGGCAATTCATTCATATGATCTGT 1671
DB 1745 CAGAGTGCAGAAAGATTTAGTCTCTCAAGGAGGGGCAATTCATTCATATGATCTGT 1804
QY 1672 GAGCTTAAAGAAATTTGTCAAAAATATAGCAAGATATCAAGTAAAGTGTAGAGGCTGT 1731
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QY 1732 CCTGATTTCTTATAGTGTGATCAACCAAGAAATTTAGAGAAAGCCCTTAAAGACTTT 1791
DB 1865 CCTGATTTCTTATAGTGTGATCAACCAAGAAATTTAGAGAAAGCCCTTAAAGACTTT 1924
QY 1792 CACATGCTGAATTTATCCGCAACAATCTCTGATGTGACCATGAGTGGTCCACCATG 1851
DB 1925 CAGATATCTGAGCTATCTGCAACACAGCTCTGATGATATCACTTGTGTCTCTGG 1984
QY 1852 CTGTGTGTGGCTGTGATCTGTGACCTTCTGATCTTCACTTGTGATCTGCTGTATCTC 1911
DB 1985 CTGTGTGTGGCTGT 2044
QY 1912 AGAGTGTGTGCTGAGTGAACCAAGTGTGGGCGCAGAGGCGCAGAACTATCCCTTAAAGAA 1971
DB 2045 AGAGTGTGTGTGCTGAGTGAACCAAGTGTGGGCGCAGAGGCGCAGAACTATCCCTTAAAGAA 2104
QY 1972 CTCGAAAGAACTTCAAGTTGATCTTATTTATATAGTAAATGATGATCTGTGCTGG 2031
DB 2105 CTCGAAAGAACTTCAAGTTGATCTTATTTATATAGTAAATGATGATCTGTGCTGG 2164
QY 2032 GTGAAAGTGAATTTGATCTTACTAGAAAAAAGATATACAGATTTGTCTTATGAG 2091
DB 2165 GTGAAAGTGAATTTGATCTTACTAGAAAAAAGATATACAGATTTGTCTTATGAG 2224
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DB 2225 AGGAACTTTGTCTGCGCAAGACATTTGTGAAAAATATCATCATGATGAGAAAGT 2284
QY 2152 TACAGTGCATCTTTGTTTGTCTCCCACTTTGTCAGAGTGTGTGCTGATTAAGAA 2211
DB 2285 TACAGTGCATCTTTGTTTGTCTCCCACTTTGTCAGAGTGTGTGCTGATTAAGAA 2344
QY 2212 CTCTATTTTGGCCATCACAATCTCTTATGAGAGATCTAATATCTTATCTCTATCTTA 2271
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DB 2405 CTGATATCCATTTCCACAGATATCTTCTGACACTACCAAGCTGAAGCTCTCATG 2464
QY 2332 AGCAGCGGACTTATTTGACAGTGTGCGCCCAAGAGAAAGCAAACTGTGGCTCTTTGGGCT 2391
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DB 2525 AACCTAAGAGCATCTTATTAATTAATCTGA 2555

RESULT 8
AKI43721 3020 bp mRNA linear HTC 21-SEP-2005
LOCUS AKI43721
DEFINITION Mus musculus 6 days neonate spleen cDNA, RIKEN full-length enriched
library, clone: F430012H09 product: toll-like receptor 1, full insert
sequence.
ACCESSION AKI43721
VERSION AKI43721.1 GI:74150781

KEYWORDS
Htc; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
1 Carninci, P. and Hayashizaki, Y.
AUTHORS
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
PUBMED
10349636
REFERENCE
2
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
PUBMED
11042159
REFERENCE
3
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)
PUBMED
11076861
REFERENCE
4
AUTHORS
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arkawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Flatschmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuell, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Stabaldi, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bul, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohlsuki, S. and Hayashizaki, Y.
CONSTRM
RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE
Functional annotation of a full-length mouse cDNA collection
JOURNAL
Nature 409 (6821), 685-690 (2001)
PUBMED
11217851
REFERENCE
5
AUTHORS
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Otsu, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bul, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanaphan, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chochia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragan, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Gilmour, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedierski, R. M., King, B. L., Konegaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Malaiz, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perce, G., Pesole, G., Petrovsky, N., Pillai, R., Portius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semp, C. A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyshaw-Boris, A., Yanagisawa, M., Yang, T., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arkawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
CONSTRM
FANTOM Consortium
TITLE
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL
Nature 420 (6915), 563-573 (2002)
PUBMED
12466851
REFERENCE
6
AUTHORS
Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M. C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V. B., Bremner, S. E., Batalov, S., Forrest, A. R., Zavolan, M., Davis, M. J., Wilming, L. G., Aldrich, V., Allen, J. E., Ambesi-Impombato, A., Apweiler, R., Attalaya, R. N., Bailey, T. L., Bansal, M., Baxter, L., Beisel, K. W., Bersano, T., Bono, H., Chalk, A. M., Chiu, K. P., Choudhary, V., Christoffels, A., Clutterbuck, D. R., Crowe, M. L., Dalla, E., Dalrymple, B. P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fegolito, M., Faulkner, G., Fletcher, C. F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T. R., Gojobori, T., Green, R. E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T. K., Hirokawa, N., Hill, D., Humnietz, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, H., Kollas, G., Krishnan, S. P., Kruger, A., Kummerfeld, S. K., Kurochkin, I. V., Lareau, L. F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan, Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mortrud, T., Muller, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K. C., Pavan, W. J., Pavese, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J. F., Ring, B. Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S. L., Sandelin, A., Schneider, C., Schonbach, C., Sekizuchi, K., Semp, C. A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Simola, B., Sperling, S., Stupka, B., Sugita, K., Sulana, R., Takenaka, Y., Taki, K., Tamoya, K., Tan, S. L., Tang, S., Taylor, M. S., Tegenka, J., Teichmann, S. A., Ueda, H. R., van Nimwegen, E., Verardo, R., Wei, C. L., Yagi, K., Yamashita, H., Zdobych, E. E., Zhu, S., Zimmer, A., Hilde, W., Bul, C., Gilmour, S. M., Teasdale, R. D., Liu, E. T., Brusic, V., Quackenbush, J., Wahlestedt, C., Matlick, J. S., Hume, D. A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori, Katayama, M., Suzuki, M., Aoki, J., Arkawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Kono, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessky, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Wachihi, A., Okamura-Ono, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
CONSTRM
FANTOM Consortium
TITLE
The transcriptional landscape of the mammalian genome
JOURNAL
Science 309 (5740), 1559-1563 (2005)
PUBMED
16141072
REFERENCE
7
AUTHORS
Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yag, C. C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K. C., Hallinan, J., Matlick, J., Hume, D. A., Lipovich, L., Batalov, S., Engstrom, P. G., Mizuno, Y., Faghli, M. A., Sandelin, A., Chalk, A. M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.
CONSTRM
RIKEN Genome Exploration Research Group
TITLE
Antisense transcription in the mammalian transcriptome
JOURNAL
Science 309 (5740), 1564-1566 (2005)
PUBMED
16141073
REFERENCE
8 (bases 1 to 3020)
AUTHORS
Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imocani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Kono, H., Murata, M., Nakamura, M., Ninomiya, N.,

Nishiiori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shiba, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Center in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse cDNAs.

FEATURES
source

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/db_xref="taxon:10090"
/clone="F430012H09"
/cissue_type="spleen"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="6 days neonate"
1..3020
/note="putative
coll-like receptor 1 (MSD) MGI:1341295 GB|AF316985,
evidence: BIASTN, 99%, match=2565)"

ORIGIN

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Best Local Similarity 68.8%; Pred. No. 8.5e-266;
Matches 1571; Conservative 0; Mismatches 706; Indels 8; Gaps 2;

139 AGAATCCAGTTCCTCCGACCGAATGATATTTGCAAGTACAGTCAAAAAGAGGCTTTAT 198
DB AAAAAATCAATTCAGAGGATGTGAGCTTATCATTAAGGCAAGCAACCTTAC 592
139 CATGTTCCAAAAGACCTGCTGAAACCAAGTCTTAGATATGTCTCAGAACTACATC 258
DB AGAGTGCCTCAAGACCTACCTTGCACCACTACTTATCTATCAAAAACATATA 652
259 GGTGAGCTTCAGGCTCTGACATGAGCTTCTATCAGATGACGTTTGAAGCTTTC 318
DB TCTGAGCTTCAGACTTCTGACATCTCTATGTCACAGCTGAGGCTCTGATTAATGTC 712
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1513 AATCTTTTAACTGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1572
DB 1913 AATCTTTTAACTGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1972
1573 GATCACAATTCAGTTTCCACCATGAGCTGATTTCTTCAAGAGTGCAGAAATGAG 1632
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1693 AATATGACCAAGATATCAAGTAAAGTAAAGGCTGATTTCTTATTAAGTGTAC 1752

QY 2403 CGCTTTAATATGAAATTAA 2422
 Db 807 ATCCATTAAATATTAACCTGA 826

RESULT 10
 DA673961 573 bp mRNA linear EST 06-NOV-2005
 LOCUS DA673961 NBRP2 Homo sapiens cDNA clone NBRP2004649 5', mRNA
 DEFINITION sequence.
 ACCESSION DA673961 GI:80920622
 VERSION DA673961.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 573)
 Kimura, K., Wakematsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

JOURNAL DB143901 564 bp mRNA linear EST 10-DEC-2005
 PUBMED DB143901 THYMU3 Homo sapiens cDNA clone THYMU3018225 5', mRNA
 COMMENT sequence.
 ACCESSION DB143901
 VERSION DB143901.1 GI:83521199
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 564)
 Kimura, K., Wakematsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
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 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

FEATURES
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QY 461 ATTCAAGGCCCTGCCATCTGTAAGAAATTGGCAACTATCACAAGTGAATTTCTTGG 520
 Db 1 ATTCAAGGCCCTGCCATCTGTAAGAAATTGGCAACTATCACAAGTGAATTTCTTGG 60

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 Db 181 AAATTCTGAATGCAAAACCTTTCACCTTGTGTTTTTCAACCAACTAGTTATTGCTATCC 240

QY 701 AAGTGAACATATCAGTTAATACCTTAGGGTGCTTACACGACTAATATTTAATTGAATG 760
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QY 761 ATGACAACCTGTCAAGTTTTCATTAAATTTTATACAGACTCAACAGAGTTCAACCTTAC 820
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QY 821 TGAATTTTACCTTCAACCAATBGAAGCAGCTTGAATGCTGTGCAAGTCTTCAAT 880
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QY 881 TTCTTTGGCCCAACCTGTGGAATATCTCAATATTACAAATTTAATTAATGAAGA 940
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QY 941 TTCTTTGGCCCAACCTGTGGAATATCTCAATATTACAAATTTAATTAATGAAGA 1000
 Db 481 TTCTTTGGCCCAACCTGTGGAATATCTCAATATTACAAATTTAATTAATGAAGA 540

QY 1001 TCACGACCAAGTTTCTGTTTTCACAGACAG 1033
 Db 541 TCACGACCAAGTTTCTGTTTTCACAGACAG 573

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 DEFINITION sequence.
 ACCESSION DB143901
 VERSION DB143901.1 GI:83521199
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 564)
 Kimura, K., Wakematsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
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 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
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JOURNAL DB143901 564 bp mRNA linear EST 10-DEC-2005
 PUBMED DB143901 THYMU3 Homo sapiens cDNA clone THYMU3018225 5', mRNA
 COMMENT sequence.
 ACCESSION DB143901
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 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Homnidae; Homo.
 1 (bases 1 to 564)
 Kimura, K., Wakematsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

FEATURES
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 Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 QY 2066 AAGATATACAGATTGTCTTCTATGAGAGAACTTTGTCCCTGGCAAGACATTGGGAAA 2125
 DB 61 AAGATATACAGATTGTCTTCTATGAGAGAACTTTGTCCCTGGCAAGACATTGGGAAA 120
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 DB 121 ATATCATCAACGTCATGAGAAAGTTACAATCCATCTTTTGTGCTCCCACTTTG 180
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 DB 181 TCCAGAGTGAAGTGTGTCATTAGAACTCTATTTTGGCCCATGCAATCTCTTTCATGAG 240
 QY 2246 GATCTAATTAACCTTAATCTCTCACTTACTCTAGAAACCATTCACAGAAACGCAATTC 2305
 DB 241 GATCTAATTAACCTTAATCTCTCACTTACTCTAGAAACCATTCACAGAAACGCAATTC 300
 QY 2306 AGTACCAACAAGCTGAAGGCTCTCATGACGACGCGACTTAATTGCAAGTGGCCCAAGAGA 2365
 DB 301 AGTACCAACAAGCTGAAGGCTCTCATGACGACGCGACTTAATTGCAAGTGGCCCAAGAGA 360
 QY 2366 AAAGCAAAAGTGGGCTCTTTTGGGCTAAACATTAGAAGCGCTTTTAATAGAAATTAAAC 2425
 DB 361 AAAGCAAAAGTGGGCTCTTTTGGGCTAAACATTAGAAGCGCTTTTAATAGAAATTAAAC 420
 QY 2426 TAGTACTGAAAAACAATGATGTGAATCTTAAAAAATTTAGAAATTTCACTTAAAGAA 2485
 DB 421 TAGTACTGAAAAACAATGATGTGAATCTTAAAAAATTTAGAAATTTCACTTAAAGAA 480
 QY 2486 CCATTATTACTTGGATGATGTGTAATAGTACGTGTAAGTACGTGTGAGGTGCT 2545
 DB 481 CCATTATTACTTGGATGATGTGTAATAGTACGTGTAAGTACGTGTGAGGTGCT 540
 QY 2546 CCATTATCCTCATGCTTCAGGAA 2569
 DB 541 CCATTATCCTCATGCTTCAGGAA 564

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 DEFINITION
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 ACCESSION DA619469
 VERSION DA619469.1 GI:80859889
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 609)

TITLE
 JOURNAL Genome Res. 16 (1), 55-65 (2006)
 PUBMED 16344360
 COMMENT Contact: Takao Isogai

FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdnalibrary.com
 NEO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction:
 Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3'-end one
 pass sequencing: RAB.

FEATURES

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ORIGIN

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 QY 62 ACATCATGACCAAGAACCAAGACCTATTTGTTAAAGCTTCATTTTGTTCCTTATGA 121
 DB 117 ACATCATGACCAAGAACCAAGACCTATTTGTTAAAGCTTCATTTTGTTCCTTATGA 176
 QY 122 TCATTAATGTTGGAACCAAGATTCAGTCTCCGACGGAATGAATTTGCACTAGACAAGT 181
 DB 177 TCATTAATGTTGGAACCAAGATTCAGTCTCCGACGGAATGAATTTGCACTAGACAAGT 236
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 DB 297 TGTCTCAGAACTAACATGCTGAGCTTCAGGTCTGTGACATGAGCTTTCTATCAGATTGA 356
 QY 302 CAGTTTGAAGCTTTCCATTAACAGAAATCCAGCTTACTGATTTAAGTCTTCAAGTTCA 361
 DB 357 CAGTTTGAAGCTTTCCATTAACAGAAATCCAGCTTACTGATTTAAGTCTTCAAGTTCA 416
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 DB 417 ACCAGATTGGAATATTGGAATTATCTCAATTAACAGTTGCAAAAAGATATCTGCGCATC 476
 QY 422 CTATTGTGAGTTTCAGGACATTGAATCTCTCATTCATATGATTTCAAGGCTCCCATCT 481
 DB 477 CTATTGTGAGTTTCAGGACATTGAATCTCTCATTCATATGATTTCAAGGCTCCCATCT 536
 QY 482 GTAAGGATTTGGCACTTATCAACAATGAAATTTCTTGGGATGAGTGTGAAAGCTGC 541
 DB 537 GTAAGGATTTGGCACTTATCAACAATGAAATTTCTTGGGATGAGTGTGAAAGCTGC 596
 QY 542 AAAAATTAGATT 554
 DB 597 AAAAATTAGATT 609

RESULT 13
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 DEFINITION 602831164f1 NCI_CGAP_C024 Mus musculus cDNA clone IMAGE:4986086 5',
 mRNA sequence.

Accession	Version	Keywords	Source	Organism
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BC963497.1	GI:14351134	EST.	Mus musculus	Mus musculus
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
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NIH-MGC http://mgc.nci.nih.gov/ .				
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strusberg, Ph.D.				
Email: cgabbs-remail.nih.gov				
Tissue Procurement: Jeffrey E. Green, M.D.				
cDNA Library Preparation: Life Technologies, Inc.				
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
DNA Sequencing by: Incyte Genomics, Inc.				
Clone distribution: MGC clone distribution information can be				
found through the I.M.A.G.E. Consortium/LLNL at:				
http://image.llnl.gov				
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High quality sequence stop: 725.				
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DB	1595	CATGGGCTGATTTCTTCCAGAGCTGCCAGAGATGAGTCAATAAAGCAGGACATC	1654	
61	CCCTGAGGATTTCTTCCAGAGCTGTCGAATATTAGTCCCTTCAACGGGAAACAAC	120		
DB	1655	CATTCATATGACCTGTGAGCTAAGAGAAATTTGCAAAATATAGACCAAGATCAATG	1714	
121	CATTCATATGACCTGTGAGCTGAGGACCTTGTCAAGAACATAGCGTGGTAGAAG	180		
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181	AAGTGTAGAGGGCTGGCTGATTTCTTAAAGTGTGACTTACCCAGAAAGTTAAGAGAA	240		
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DB	1835	CCATCGGTGACCATGCTGAGTGTGGCTGTGACCTGATACCTGCTGATCACTTGG	1894	
301	CCATCGGTGACCATGCTGAGTGTGGCTGTGACCTGATACCTGCTGATCACTTGG	360		
DB	1895	ATCTGCTGATATCTCAGATGTGTGCCAGTGAACCAAGCTGGCGCAGGGCCAGGA	1954	
361	ACCTGCTGATATGTGAGATGTGTGTGATGATGATGATGATGATGATGATGATGATG	420		
DB	1955	ACATACCTTGAAGAACTCCAAAGAAACCTCCAGTTTCAAGCTTTATTTATTTATG	2014	
421	ACATACCTTGAAGAACTCCAAAGAAACCTCCAGTTTCAAGCTTTATTTATTTATG	480		

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QY <td>541</td> <td>AGATTGTCCTTCATGAGAGAACTTTGTCCCTGGCAAGACATGTGTGAGAAATCATCA</td> <td>600</td>	541	AGATTGTCCTTCATGAGAGAACTTTGTCCCTGGCAAGACATGTGTGAGAAATCATCA	600
Db <td>2135</td> <td>ACTGCATTGAGAGAGTTCACAAAGTCATCTTTGTGTTGTCTCCCAACTTTGTCCAGAGTG</td> <td>2194</td>	2135	ACTGCATTGAGAGAGTTCACAAAGTCATCTTTGTGTTGTCTCCCAACTTTGTCCAGAGTG	2194
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QY <td>721</td> <td>AACTTAATCTCATCTTGCTGGCA-CCATACCCGAGTCTGAGTCCCTACAA</td> <td>772</td>	721	AACTTAATCTCATCTTGCTGGCA-CCATACCCGAGTCTGAGTCCCTACAA	772

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		698 bp	mRNA	linear	EST 16-MAR-2004	

REFERENCE	1 (bases 1 to 698)
AUTHORS	Sonstegard, T.S., Van Tassel, C.P., Metukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
TITLE	Production of EST from cDNA libraries derived from immunologically activated bovine gut
JOURNAL	Unpublished (2004)
COMMENT	Contact: Tad S. Sonstegard Bovine Functional Genomics Laboratory Animal and Natural Resources Institute Bldg. 200 Rm2a BARC-East, Beltsville, MD 20705, USA Tel: 3015048416 Fax: 3015048414 Email: tads@anri.barc.usda.gov Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim alt "-trim fasta. Vector identified by cross match using options -mismatch 12 -mismatch 12 Plate: 41 row: D column: 08 Seq primer: CCCAGTCACGACGTTGTTAAACG High quality sequence stop: 698. Location/Qualifiers

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Fri Jun 9 14:07:32 2006

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